

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 22:55:45 ; Search time 3287 Seconds
(without alignments)
9615.138 Million cell updates/sec

Title: US-10-686-428A-3_COPY_444_999

Perfect score: 556

Sequence: 1 aaggagctcatggcgcg.....catcagccagtggaaggga 556

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sy.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	100.0	3000	4 SSPAI1	Y11347 S.scrofa mr
2	480.8	86.5	2970	4 BTPAI1MR	X16383 Bovine mRNA
3	461.2	82.9	844	4 AF508034	AF508034 Equus cab
4	455.2	81.9	1209	11 AY888695	AY888695 Synthetic
5	455.2	81.9	1209	11 AY889067	AY889067 Synthetic
6	455.2	81.9	1209	11 AY891356	AY891356 Synthetic
7	455.2	81.9	1209	11 AY891655	AY891655 Synthetic
8	455.2	81.9	1209	11 AY893400	AY893400 Synthetic
9	455.2	81.9	1209	11 AY893851	AY893851 Synthetic
10	455.2	81.9	1532	6 CQ716284	CQ716284 Sequence
11	455.2	81.9	1362	8 HSPAIR1	X04744 Human mRNA
12	455.2	81.9	2207	8 BC010860	BC010860 Homo sapi
13	455.2	81.9	2660	6 CQ413075	CQ413075 Sequence
14	455.2	81.9	2876	6 AR106060	AR106060 Sequence
15	455.2	81.9	2876	6 AR106066	AR106066 Sequence
16	455.2	81.9	2876	6 BD094083	BD094083 Shear str
17	455.2	81.9	2876	6 CQ776713	CQ776713 Sequence
18	455.2	81.9	2876	6 AR258505	AR258505 Sequence

c

c	19	455.2	81.9	2876	6	AR258511	Sequence
	20	455.2	81.9	2876	6	AR380642	Sequence
	21	455.2	81.9	2876	6	AX156115	Sequence
	22	455.2	81.9	2876	8	HUMPAI	Human plasm
	23	455.2	81.9	2937	6	CQ861596	Sequence
	24	455.2	81.9	2937	8	HUMPAIB	Human beta-
	25	455.2	81.9	2944	6	I08667	Sequence
	26	455.2	81.9	3171	6	AX281751	Sequence
	27	453.6	81.6	1209	11	AY891093	AY891093 Synthetic
	28	453.6	81.6	1482	6	AX787059	Sequence
	29	453.6	81.6	1482	8	HSPAIR	Human mRNA
	30	452	81.3	2970	4	MVPAI1	X58541 Mink mRNA
	31	447.2	80.4	1187	6	CQ785751	Sequence
	32	447.2	80.4	1187	6	CQ795516	Sequence
	33	447.2	80.4	1209	8	AF393201	Cercopith
	34	447.2	80.4	1482	8	HSENDPAI	X12701 H.sapiens m
	35	426.8	76.8	548	4	AF074325	Oryctolag
	36	420	75.5	3053	6	AX827499	Sequence
	37	420	75.5	3053	9	RATPAI1a	AX827499 Sequence
	38	415.2	74.7	2741	9	BC054091	M24067 Rattus norv
	39	412	74.1	2999	6	CQ777582	BC054091 Mus muscu
	40	412	74.1	2999	9	MUSPAI1	CQ777582 Sequence
	41	294.4	52.9	1155	6	BD091054	M33960 Mouse plasm
	42	286.2	51.5	9360	8	HSM809316	BD091054 DNA chip
	43	218.6	39.3	249	4	BTPAI1	EX649164 Homo sapi
	44	213.4	38.4	263	4	AF069712	X52906 Bovine PAI-
	45	172.8	31.1	246	6	CQ054952	AF069712 Oryctolag

ALIGNMENTS

RESULT 1	SSPAI1	3000 bp	mRNA	linear	MAM 18-APR-2005
LOCUS	S.scrofa mRNA for plasminogen activator inhibitor-1.				
DEFINITION	Y11347.1 GI:1870169				
ACCESSION	Y11347.1				
VERSION	PAI-1 protein; PLANH1 gene; plasminogen activator inhibitor-1.				
KEYWORDS	Sus scrofa (pig)				
SOURCE	Sus scrofa				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.				
REFERENCE	1				
AUTHORS	Bijlens A.P., Knockaert, I., Cousin, E., Kruihof, E.K. and Declerck, P.J.				
TITLE	Expression and characterization of recombinant porcine plasminogen activator inhibitor-1				
JOURNAL	Thromb. Haemost. 77 (2), 350-356 (1997)				
PUBMED	9157595				
REFERENCE	2 (bases 1 to 3000)				
AUTHORS	Kruihof, E.K.O.				
TITLE	Direct Submission				
JOURNAL	Submitted (18-FEB-1997) E.K.O. Kruihof, Division of Angiology and Hemostasis, University Hospital Geneva, CH-1211 Geneva, SWITZERLAND				
FEATURES	Location/Qualifiers				
source	1..3000				
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	/mol_type="mRNA"				
	/db_xref="taxon:9823"				
	/cell_type="thoracic artery cells"				
	/clone_lib="Stratagene, cat no 937700"				
gene	1..3000				
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CDS	/note="plasminogen activator inhibitor I"				
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	/protein_id="CAA72182.1"				
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	/db_xref="GOA:P79335"				

/db_xref="UniProt/Swiss-Prot:P79335"
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/gene="PLANHI"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3e-120;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGGTGGGAACAAAGATGATCAGCACGGCCGATGCCATCTTCGTG 60
DB 444 AAGGAGCTCATGGGCGGTGGGAACAAAGATGATCAGCACGGCCGATGCCATCTTCGTG 503
QY 61 CAGCGGATCTGAAGTGTCTCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCGGACC 120
DB 504 CAGCGGATCTGAAGTGTCTCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCGGACC 563
QY 121 ACAGTCAGCAGTGTGATTTTCAGAGTGGACAGACGAGCTTCATCATCAATCACTGG 180
DB 564 ACAGTCAGCAGTGTGATTTTCAGAGTGGACAGACGAGCTTCATCATCAATCACTGG 623
QY 181 GTGAAGAGACACACAAAGGCGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCAG 240
DB 624 GTGAAGAGACACACAAAGGCGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCAG 683
QY 241 CTGACGGCTGTGTGTGAATGCCCTCTACTTCAACGGCCAGTGGAAACGCCCTTC 300
DB 684 CTGACGGCTGTGTGTGAATGCCCTCTACTTCAACGGCCAGTGGAAACGCCCTTC 743
QY 301 CCAGAGAAAGACACACACGGCTCTCCACAGTCTGATGGCAGCACCGTCTCTGTG 360
DB 744 CCAGAGAAAGACACACACGGCTCTCCACAGTCTGATGGCAGCACCGTCTCTGTG 803
QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACACTGATTTTCCACCCCGAGCGCAT 420
DB 804 CCATGATGGCTCAGACCAACAAAGTTCAACTACACTGATTTTCCACCCCGAGCGCAT 863
QY 421 TACTAGACATCTCTGAATGTCCTTACACGGCAACACTCTGAGCATGTTCAATTCGGCC 480
DB 864 TACTAGACATCTCTGAATGTCCTTACACGGCAACACTCTGAGCATGTTCAATTCGGCC 923
QY 481 CCTACGAAAGAGTGCTCTCTCCGCTCACCAGCATCTCGAGCATGTTCAATTCGGCC 540
DB 924 CCTACGAAAGAGTGCTCTCTCCGCTCACCAGCATCTCGAGCATGTTCAATTCGGCC 983
QY 541 AGCCAGTGAAGAGGA 556
DB 984 AGCCAGTGAAGAGGA 999

RESULT 2

BTPA11MR 2970 bp mRNA linear MAM 18-APR-2005
LOCUS BTPA11MR
DEFINITION Bovine mRNA for Plasminogen activator inhibitor (PAI-1).
ACCESSION X16383
VERSION X16383.1 GI:600
KEYWORDS PAI-1 gene; plasminogen activator inhibitor; plasminogen activator inhibitor type 1.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 2970)

AUTHORS Mimuro,J., Sawdey,M., Hattori,M. and Luskutoff,D.J.
TITLE cDNA for bovine type 1 plasminogen activator inhibitor (PAI-1)
JOURNAL Nucleic Acids Res. 17 (21), 8872 (1989)
PUBMED 2587231
REFERENCE 2 (bases 1 to 2970)
AUTHORS Sawdey,M.S.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-1989) Sawdey M.S., Research Institute of Scripps
Clinic, 10666 No Torrey Pines Road, La Jolla CA 92014, U S A
FEATURES
source
1..2970
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/cell_line="aortic endothelial"
122..1330
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/product="plasminogen activator inhibitor"
/protein_id="CAA34419.1"
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/db_xref="InterPro:IPR000215"
/db_xref="UniProt/Swiss-Prot:P13909"
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DMVKRHTKGMINDLLGQGAVDQTLRLVLAALYFNQWKPFPPEKSTHRLPHKSDGS
TVSPMMAQTNKFNTEFTPDGHYDILELPHYGNLTSMFETAAPEYKHEVPLSALTSI
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122..190
sig_peptide
mat_peptide 191..1327
/product="plasminogen activator inhibitor"
1226..1231
misc_feature
/note="reactive center"
1442..1453
misc_feature
/note="mRNA regulatory signal (AUUU)"

Query Match 86.5%; Score 480.8; DB 4; Length 2970;
Best Local Similarity 91.5%; Pred. No. 1.5e-103;
Matches 509; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGGTGGGAACAAAGATGATCAGCACGGCCGATGCCATCTTCGTG 60
DB 428 AAGGAGCTCATGGGCGGTGGGAACAAAGATGATCAGCACGGCCGATGCCATCTTCGTG 487
QY 61 CAGCGGATCTGAAGTGTCTCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGACC 120
DB 488 CAGCGGATCTGAAGTGTCTCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGACC 547
QY 121 ACAGTCAGCAGTGTGATTTTCAGAGATGACAGACGAGCTTCATCATCAATCACTGG 180
DB 548 ACAGTCAGCAGTGTGATTTTCAGAGATGACAGACGAGCTTCATCATCAATCACTGG 607
QY 181 GTGAAGAGACACACAAAGGCGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCAG 240
DB 608 GTGAAGAGACACACAAAGGCGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCAG 667
QY 241 CTGACGGCTGTGTGTGAATGCCCTCTACTTCAACGGCCAGTGGAAACGCCCTTC 300
DB 668 CTGACGGCTGTGTGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGTGGCCCTTC 727
QY 301 CCAGAGAAAGACACTCACCGCTCTTCCAAAGTCTGATGGCAGCACCGTCTCTGTG 360
DB 728 CCAGAGTCAAAACACCCACCGCTCTTCCAAAGTCCGATGGCAGCACCATCTCTGTG 787
QY 361 CCCATGATGGCTCAGACCAACAAAGTCAACTGAGTTTCCACCCCGAGCGCAT 420
DB 788 CCCATGATGGCTCAGACCAACAAAGTCAACTGAGTTTACACCCCGAGCGCAT 847
QY 421 TACTACGACATCTCTGAATTTGCCCTTACCAACGGCAACACTCTGAGCATGTTCAATTCGCCGC 480

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Db      848  TACTACGACATCTTGGAAATTCCTTACCAAGGAGGCGCTTCTCAGAGTCTCAGTCTGCC 907
QY      481  CCCTACGAAAGAGGTGCTTCTCTCGCCCTCAGCAGCATCTTGGAGCTCAGCTCATC 540
Db      908  CCCTATGAGAGAGGAGTGCCTCTCTGCCCCTCACCAGCATCTTGGAGTCTGAGCTCATC 967
QY      541  AGCCAGTGGAAAGGGA 556
Db      968  AGCCAGTGGAAAGGGA 983

RESULT 3
AF508034
LOCUS   AF508034      844 bp      mRNA      linear      MAM 22-MAY-2002
DEFINITION   Equus caballus plasminogen activator inhibitor-1 (PAI-1) mRNA,
partial cds.
ACCESSION   AF508034
VERSION     AF508034.1 GI:21070317
KEYWORDS    Equus caballus (horse)
SOURCE      Equus caballus
ORGANISM    Equus caballus
REFERENCE   1 (bases 1 to 844)
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiathiria; Perissodactyla; Equidae; Equus.
TAKAFUJI, V.A., Sharova, L.V., Crisman, M.V. and Howard, R.D.
TITLE      Direct Submission
JOURNAL    Submitted (01-MAY-2002) Large Animal Clinical Sciences, Orthopedic
Research Laboratory, VA-MD Regional College of Veterinary Medicine,
Virginia Polytechnic Institute and State University, Duckpond
Drive, Blacksburg, VA 24061, USA

FEATURES             Location/Qualifiers
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                     /organism="Equus caballus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9796"
                     /tissue_type="equine IL-1 stimulated synovium"
                     /note="RT-PCR amplified using degenerate upper primer:
5'-GGG(CG)CC(GA)TGGACAA(GA)GATGAGAT-3', and lower primer:
5'-TGGCG(CGA)ACCAC(GA)AA(GC)AG-3'"
     gene             <1..>844
     CDS              <1..>844
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                     /codon_start=3
                     /product="plasminogen activator inhibitor-1"
                     /protein_id="AAM34252.1"
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EVLPSALTNIIDLAQLISQWKRSMTRVRLVLPKFSLESDVLRRLPLENLGMDMPRP
NOADFTTSGNQLLHVSQLQVKIEVTESGTVASSSTGFVSARMAPEIIMDRFL
FVVR"

ORIGIN
Query Match      82.9%; Score 461.2; DB 4; Length 844;
Best Local Similarity 90.3%; Pred. No. 6.3e-98;
Matches 493; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY      11  TGGGCGCGTGGACAAGATGAGATCAGACGCGCCATGCGATCTTCGTCAGCGGGATC 70
Db      1  TGGGCGCGTGGACAAGATGAGATCAGACGCGCCATGCGATCTTCGTCAGCGGGATC 60
QY      71  TGAAGCTGGTCCAGGGTTTCTATCCCTACTTCTTCAGGCTGTTCGGACACCGTCAAGC 130
Db      61  TGAAGCTGGTCAAGGAATTCATGCCCGCTTCTTCAAGCTGTTCACACACAGTCAAGC 120
QY      131  AGGTGGATTTTTCAGAGATGGACAGACCGCAGGTTCATCATCATGATCGGTGGAGAGAC 190
Db      121  AGGTGGACTTTTTCAGAGGTGGAGAGACCGCAGGTTCATCATCATGATCGGTGGAGAAAT 180
QY      191  ACACAAAGGCATGATCAATGACTTACTTTGGCCAAAGGGGCTGTGGACCAGCTGACGCGCC 250

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Db      181  ACACAAAGGCATGATCAGCGACTTACTTGACGAAGGGGCGTGGACGAGCTGACGCGCC 240
QY      251  TGGTTCGTGTAATGCGCTTACTTTCAACGCGCAGTGGAAACCGCCCTTCCAGAGAAAA 310
Db      241  TGGTGTGTAATGCGCTTACTTTCAACGCGCAGTGGAAACCGCCCTTCCAGAGTCGG 300
QY      311  GCATCTACCAACCGCTTCTTCCAAAGTCTGATGCGACGACCGTCTCTGTGCCCCATGATGG 370
Db      301  GCACCCACCAACCGCTTCTTCCAAAGTCTGATGCGACGACCGCTCTGTGTCCATGATGG 360
QY      371  CTCAGACCAACAAGTTCAACTACACTGAGTTCAGTTCCTCCACCCCGGAGCGGCATTACTACGACA 430
Db      361  CTCAGACCAACAAGTTCAACTATGCTGAGTTTACCACCCCTGACGCGCATTTACTACGACA 420
QY      431  TCCTGGAATTCGCCCTTACCACGCGCAACACTCTGAGCATGTTTCATTGGCGGCCCTTACGAAA 490
Db      421  TCCTGGAATTCGCCCTTACCACGCGGACACCTCTGAGCATGTTTCATTGGCGCTCCCTATGAAA 480
QY      491  AAGAGTGCCCTCTCTCGGCCCTCACGAGCATTTGGACGCTCAGCTCATCAGCCAGTGGGA 550
Db      481  AAGAGTGCCCTCTCTCTGCCCCCTCACCACCATTTCTGGATGCCAGCTCATCAGCCAGTGGGA 540
QY      551  AAGGGA 556
Db      541  AAGGGA 546

RESULT 4
AY888695
LOCUS   AY888695      1209 bp      mRNA      linear      SYN 22-MAR-2005
DEFINITION   Synthetic construct Homo sapiens clone FLH031026.01X serine or
cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
complete cds.
ACCESSION   AY888695
VERSION     AY888695.1 GI:61358892
KEYWORDS    Human ORF Project.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 1209)
AUTHORS    Hines, L., Rolfs, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.
TITLE      Cloning of human full-length CDS in Creator (TM) recombinational
vector system
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 1209)
AUTHORS    Hines, L., Rolfs, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.
TITLE      Direct Submission
JOURNAL    Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
COMMENT    This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned with normalized stop-codon. The CDS
has been directionally cloned using ED in-Fusion(TM) cloning system
between the SalI and HindIII sites of the pBMR-dual vector.
Additional sequences in the clone: 'ACC' after SalI site and
before 'ATG' to provide Kozak consensus sequence. Each clone is
clonally isolated and full-length sequence-verified.
FEATURES             Location/Qualifiers
     source           1..1209
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
                     /clone="FLH031026.01X"
                     /lab_host="Escherichia coli DH5alpha Tl resistant"
                     /note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
     gene             1..1209

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Db GTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCGGTGACCCAG 546
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 Db 547 CTGACAGCGCTGGTGGTGAATGCTTACTTCAACGCCAGTGGAAAACGCCCTTC 606
 QY 301 CCAGAGAAAAGCACTCAACACCGGCTCTTCCACAAGTCTGATGCGACGCGTCTCTGTG 360
 Db 607 CCCGACTCCAGCACCCACCGCGCTCTTCCACAAGTCTGATGCGACGCGTCTCTGTG 666
 QY 361 CCATGATGCTCAGACCAACAAGTCAACTACACTGAGTTTCCACCCCGACGGCCAT 420
 Db 667 CCATGATGCTCAGACCAACAAGTCAACTACACTGAGTTTCCACCCCGACGGCCAT 726
 QY 421 TACTACACATCTGGTAATGCTTCAACCGGCAACTCTGAGCATGTTCAATGCGGCC 480
 Db 727 TACTACACATCTGGTAATGCTTCAACCGGCAACTCTGAGCATGTTCAATGCGGCC 786
 QY 481 CCTTACAAAAGAGGTGCTCTCTCCGCTCTACACAGCATTTGAGCGCTCAGCTCATC 540
 Db 787 CCTTATGAAAAGAGGTGCTCTCTCTGCTCTCACCACATTTGAGTGGCCAGCTCATC 846
 QY 541 AGCCAGTGGAAAGGGA 556
 Db 847 AGCCACTGGAAAGGCA 862

RESULT 6
 AY891356
 LOCUS
 DEFINITION
 1209 bp mRNA linear SYN 21-MAR-2005
 Synthetic construct Homo sapiens clone FLH031022.01L serine or
 cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
 partial cds.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 AY891356
 AY891356.1 GI:61369090
 Human ORF Project.
 synthetic construct
 synthetic construct
 other sequences; artificial sequences.

REFERENCE
 AUTHORS
 1 (bases 1 to 1209)
 Hines, L., Rolfs, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F.,
 Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
 Williamson, J. and Labaer, J.
 Cloning of human full-length CDS in Creator (TM) recombinational
 vector system

JOURNAL
 REFERENCE
 AUTHORS
 2 (bases 1 to 1209)
 Hines, L., Rolfs, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F.,
 Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
 Williamson, J. and Labaer, J.

TITLE
 JOURNAL
 Submitted (05-JAN-2005) Biological Chemistry and Molecular
 Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
 Cambridge, MA 02141, USA

COMMENT
 This CDS clone is a part of a collection of human full-length
 expression clones generated by Harvard Institute of Proteomics.
 This ORF clone has been cloned without stop-codon (to allow fusion
 with C-terminal tag). The CDS has been directionally cloned using
 BD In-Fusion(TM) cloning system between the SalI and HindIII sites
 of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'
 after SalI site and before 'ATG' to provide Kozak consensus
 sequence; 'GG' after last codon and before HindIII site to maintain
 reading frame. Each clone is clonally isolated and full-length
 sequence-verified.

FEATURES
 source
 Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 /clone="FLH031022.01L"
 /lab_host="Escherichia coli DH5alpha T1 resistant"
 /note="derived from Homo sapiens first strand cDNA library"

from placenta and brain
 1..>1209
 /gene="SERPINE1"
 1..>1209
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 /notes="nexin; plasminogen activator inhibitor type 1"
 /codon_start=1
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 member 1"
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 /db_xref="GI:61369091"
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 TVSPNMAQTNKFTYFTPDGHYDILELPHYGDITLSMFIAPAEKVEKPLSALTNI
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ORIGIN

Query Match 81.9%; Score 455.2; DB 11; Length 1209;
 Best Local Similarity 88.7%; Pred. No. 1.6e-96;
 Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCTGGAAACAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 60
 Db 307 AAGGAGCTCATGGGCGCTGGAAACAAGATGAGATCAGACGCGCGATCTTCGTG 366
 QY 61 CAGCGGATCTGAGCTGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCCGGACC 120
 Db 367 CAGCGGATCTGAGCTGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCCGGACC 426
 QY 121 ACGGTCAGACGCTGATTTTTCAGAGATGGACAGCCAGGTTTCATCATCATGACTGG 180
 Db 427 ACGGTCAGACGCTGATTTTTCAGAGATGGACAGCCAGGTTTCATCATCATGACTGG 486
 QY 181 GTGAAGAGACACACAAAAGGCTATGATCAATGACTTCTTGGCCAAAGGGCTGTGGACCAG 240
 Db 487 GTGAAGAGACACACAAAAGGCTATGATCAATGACTTCTTGGCCAAAGGGCTGTGGACCAG 546
 QY 241 CTGACGCGCTGTTCTGTTGTAATGCCCTTCTTCAACGCGCAGTGGAAAACGCCCTTC 300
 Db 547 CTGACGCGCTGTTCTGTTGTAATGCCCTTCTTCAACGCGCAGTGGAAAACGCCCTTC 606
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 Db 607 CCAGACTCCAGCACCCACCGCGCTCTTCCACAAGTCTGATGCGACGCGCTCTCTGTG 666
 QY 361 CCATGATGCTCAGACCAACAAGTCAACTACACTGAGTTTTCACCCCGACGGCCAT 420
 Db 667 CCATGATGCTCAGACCAACAAGTCAACTACACTGAGTTTTCACCCCGACGGCCAT 726
 QY 421 TACTACGACATCTGGAATGCCCTTACACGGCAACACTCTGAGCATGTTCAATGCGGCC 480
 Db 727 TACTACGACATCTGGAATGCCCTTACACGGGGACACCTCAGCATGTTCAATGCGGCC 786
 QY 481 CCTTACAAAAGAGGTGCTCTCTCCGCTCTACACAGCATTTGAGACGCTCAGCTCATC 540
 Db 787 CCTTATGAAAAGAGGTGCTCTCTCTGCTCTCACCACATTTGAGTGGCCAGCTCATC 846
 QY 541 AGCCAGTGGAAAGGGA 556
 Db 847 AGCCACTGGAAAGGCA 862

RESULT 7

AY891655
 LOCUS
 DEFINITION
 1209 bp mRNA linear SYN 29-MAR-2005
 Synthetic construct Homo sapiens clone FLH016836.01L serine or
 cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
 partial cds.

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ACCESSION AY891655
VERSION AY891655.1 GI:61370956
KEYWORDS Human ORF Project.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1209)
AUTHORS Hines,L., Rolfs,A., Jepsen,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and Labaer,J.
TITLE Cloning of human full-length CDS in Creator (TM) recombinational
vector system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1209)
AUTHORS Hines,L., Rolfs,A., Jepsen,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and Labaer,J.
Direct Submission
Submitted (05-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). The CDS has been directionally cloned using
BD In-Fusion(TM) cloning system between the SalI and HindIII sites
of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'
after SalI site and before 'ATG' to provide Kozak consensus
sequence; 'GG' after last codon and before HindIII site to maintain
reading frame. Each clone is clonally isolated and full-length
sequence-verified.
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                VLFMGQVMEPL"
ORIGIN
Query Match 81.9%; Score 455.2; DB 11; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGGTGGAAACAGATGATCAGCAGCGCGCATCTTCGTG 60
Db 307 AAGGAGCTCATGGGCGGTGGAAACAGATGATCAGCAGCGCGCATCTTCGTG 366
QY 61 CAGCGGGATCTGAAGCTGTCCAGGGTTTCATGCCCTCTTCAGGCTGTTCGGACC 120
Db 367 CAGCGGGATCTGAAGCTGTCCAGGGTTTCATGCCCTCTTCAGGCTGTTCGGACC 426
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTCATCATCAATGACTGG 180

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Db 427 ACGGTCAAGCAGGTGGATTTTTCAGAGGTGGAGAGCCAGATTTCATCATCAATGACTGG 486
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QY 241 CTGACGCGCCTGGTTCGTGGTGAATGCCCTTACTTCAACGGCCAGTGGAAACGCCCTTC 300
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QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTACACTGTAGTTTTCACCCCGCAGCGCCAT 420
Db 667 CCCATGATGGCTCAGACCAACAAGTTCAACTACACTGTAGTTTTCACCCCGCAGCGCCAT 726
QY 421 TACTACGACATCTCTGGAAATTCCTTACCACGGCAACACTCTGAGCATGTTCATTCGCGCC 480
Db 727 TACTACGACATCTCTGGAAATTCCTTACCACGGCAACACTCTGAGCATGTTCATTCGCGCC 786
QY 481 CCCTACGAAAAGAGGTGCTCTCTCCGCCCTCACCAGCATCTTGGACGCTCAGTCTCATC 540
Db 787 CTTATGAAAAAAGAGGTGCTCTCTCTGCCCTCACCACATTTCTGAGTGGCCAGCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCAGTGGAAAGGGA 862

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RESULT 8
AY893400 1209 bp mRNA linear SYN 16-MAR-2005
LOCUS AY893400
DEFINITION Synthetic construct Homo sapiens clone FLH057235.01X serine or
cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
complete cds.
ACCESSION AY893400
VERSION AY893400.1 GI:60817775
KEYWORDS Human ORF Project.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1209)
AUTHORS Hines,L., Taron,B., Jepsen,D., Moreira,D., Raphael,J., Shen,B.,
Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and Labaer,J.
TITLE Cloning of human full-length CDS FLEXGene in
Gateway(TM) recombinational vector system
Unpublished
JOURNAL 2 (bases 1 to 1209)
REFERENCE Hines,L., Taron,B., Jepsen,D., Moreira,D., Raphael,J., Shen,B.,
Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and Labaer,J.
AUTHORS Direct Submission
TITLE Submitted (04-JAN-2005) Biological Chemistry and Molecular
JOURNAL Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
COMMENT This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned with normalized stop-codon. AttB
recombination sites have been added to either end of the ORF and
directionally cloned using the Gateway cloning system into pDONR
201. Additional sequences in the clone: 'ACC' before the 'ATG'
(corresponding to ribosomal binding site and Kozak consensus
sequences). Each clone is clonally isolated and full-length
sequence-verified.
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        Location/Qualifiers
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partial cds.
AY893851 GI:60829666
Human ORF Project.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 1209)
Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D., and LaBaer, J.
Cloning of human full-length CDS FLEXGene in
Gateway(TM) recombinational vector system
Unpublished
2 (bases 1 to 1209)
Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D., and LaBaer, J.
Direct Submission
Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
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This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). AttB recombination sites have been added to
either end of the ORF and directionally cloned using the Gateway
cloning system into pDONR 201. Additional sequences in the clone:
'ACC' before the 'ATG' (corresponding to ribosomal binding site and
Kozak consensus sequences). Each clone is clonally isolated and
full-length sequence-verified.
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from placenta and brain"
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VLFMGQVMEPL"
ORIGIN
Query Match 81.9%; Score 455.2; DB 11; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTATGGGGCGTGGAAACAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
DB 307 AAGGAGCTATGGGGCGTGGAAACAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 366
QY 61 CAGCGGGATCTGAAGCTGTGCAGGGTTTCATGCCCTACTTCTTCCAGCTGTTCGGACC 120
DB 367 CAGCGGGATCTGAAGCTGTGCAGGGTTTCATGCCCTACTTCTTCCAGCTGTTCGGACC 426
QY 121 ACGGTCAAGCAGTGTGATTTTTCAGAGATGGACAGACGGCAGGTTTCATCATCAATGACTG 180
DB 427 ACGGTCAAGCAGTGTGATTTTTCAGAGATGGACAGACGGCAGGTTTCATCATCAATGACTG 486
QY 181 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCAGGGGCTGTGGACACCA 240
DB 487 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCAGGGGCTGTGGACACCA 546
QY 241 CTGACGGCTGTGTTCTGTGATGCCCTTACTTCAACGGCCAGTGGAAAGCGCCCTTC 300
DB 547 CTGACGGCTGTGTTCTGTGATGCCCTTACTTCAACGGCCAGTGGAAAGCGCCCTTC 606
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCCAAGTCTGTGATGGCAGCCGCTCTCTGTG 360
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DB 667 CCCATGATGGCTCAGACCAACAGTTCACACTACATGAGTTTTCACCCCGCAGCGCCAT 726
QY 421 TACTACGATCTGGAATGGCTTACACAGGCAACACTCTGAGCATGTTCAATGCCGCC 480
DB 727 TACTACGATCTGGAATGGCTTACACAGGCAACACTCTGAGCATGTTCAATGCCGCC 786
QY 481 CCTACGAAAAGAGTGCTCTCTCCGCCCTCACAGCATTTCTGAGCGCTCAGCTCATC 540
DB 787 CTTTATGAAAAGAGTGCTCTCTCTCCGCCCTCACAGCATTTCTGAGTGCCCGCAGCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
DB 847 AGCCAGTGGAAAGGCA 862
RESULT 9
AY893851
LOCUS
DEFINITION
Synthetic construct Homo sapiens clone FLH057231.01L serine or
cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
1209 bp mRNA linear SYN 16-MAR-2005

partial cds.
AY893851 GI:60829666
Human ORF Project.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 1209)
Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D., and LaBaer, J.
Cloning of human full-length CDS FLEXGene in
Gateway(TM) recombinational vector system
Unpublished
2 (bases 1 to 1209)
Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D., and LaBaer, J.
Direct Submission
Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned without stop-codon (to allow fusion
with C-terminal tag). AttB recombination sites have been added to
either end of the ORF and directionally cloned using the Gateway
cloning system into pDONR 201. Additional sequences in the clone:
'ACC' before the 'ATG' (corresponding to ribosomal binding site and
Kozak consensus sequences). Each clone is clonally isolated and
full-length sequence-verified.
Location/Qualifiers
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/db_xref="taxon:32630"
/clone="FLH057231.01L"
/lab_host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
gene
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CDS
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VLFMGQVMEPL"
ORIGIN
Query Match 81.9%; Score 455.2; DB 11; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTATGGGGCGTGGAAACAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
DB 307 AAGGAGCTATGGGGCGTGGAAACAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 366
QY 61 CAGCGGGATCTGAAGCTGTGCAGGGTTTCATGCCCTACTTCTTCCAGCTGTTCGGACC 120
DB 367 CAGCGGGATCTGAAGCTGTGCAGGGTTTCATGCCCTACTTCTTCCAGCTGTTCGGACC 426
QY 121 ACGGTCAAGCAGTGTGATTTTTCAGAGATGGACAGACGGCAGGTTTCATCATCAATGACTG 180
DB 427 ACGGTCAAGCAGTGTGATTTTTCAGAGATGGACAGACGGCAGGTTTCATCATCAATGACTG 486
QY 181 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCAGGGGCTGTGGACACCA 240
DB 487 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCAGGGGCTGTGGACACCA 546
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QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCCAAGTCTGTGATGGCAGCCGCTCTCTGTG 360
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QY 361 CCCATGATGGCTCAGACCAACAGTTCACACTACATGAGTTTTCACCCCGCAGCGCCAT 420
DB 667 CCCATGATGGCTCAGACCAACAGTTCACACTACATGAGTTTTCACCCCGCAGCGCCAT 726
QY 421 TACTACGATCTGGAATGGCTTACACAGGCAACACTCTGAGCATGTTCAATGCCGCC 480
DB 727 TACTACGATCTGGAATGGCTTACACAGGCAACACTCTGAGCATGTTCAATGCCGCC 786
QY 481 CCTACGAAAAGAGTGCTCTCTCCGCCCTCACAGCATTTCTGAGCGCTCAGCTCATC 540
DB 787 CTTTATGAAAAGAGTGCTCTCTCTCCGCCCTCACAGCATTTCTGAGTGCCCGCAGCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
DB 847 AGCCAGTGGAAAGGCA 862
RESULT 9
AY893851
LOCUS
DEFINITION
Synthetic construct Homo sapiens clone FLH057231.01L serine or
cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
1209 bp mRNA linear SYN 16-MAR-2005

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487	Db	GTGAAGACACACACAA	AAAGGTATGATCAGCA	ACTTGTCTTGGAAAGGAG	CGCGTGGACCAG 546
241	Qy	CTGACGCGCTGGTTCT	TGGTGAATGCCCTCT	ACTTCTCAACGGCCAGT	TGAAAAACGCCCTTC 300
547	Db	CTGACACGGCTGGTGT	GGTGAATGCCCTCT	ACTTCTCAACGGCCAGT	TGAAAGACTCCCTTC 606
301	Qy	CCAGAAAAAGCACTCA	CCACCGCCTCTTCC	ACAAGTCTGATGGCAG	CACCGTCTCTCTGTG 360
607	Db	CCGACTCTCAGCACCC	ACCGCGCGCTCTT	CCACAAATCAGACGG	CAGCACTGTCTCTGTG 666
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667	Db	CCCATGATGGCTCAG	ACCAACAAAGTT	CAAACTATACTGAG	TTTCAACGCGCCGATGGCCAT 726
421	Qy	TACTACACATCCTGG	AATGCCCTACACGG	CAACACTCTGAGCAT	GTTCATTGCGCGCC 480
727	Db	TACTACACATCCTGG	AATGCCCTACACGG	GACACCCCTCAGCAT	GTTCATTGCTGCC 786
481	Qy	CCCTACAAAAAGAG	GTGCCTCTCTCGC	CCCTCACCAGCA	CTTCTGGAGCCTCAGCTCATC 540
787	Db	CCTTATGAAAAAG	AGGTGCCTCTCT	CTGCGCCTCACCA	ACATCTCTGAGTGCCAGCTCATC 846
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847	Db	AGCCACTGGAAAGGA	862		

RESULT 10	
LOCUS	CQ716284
DEFINITION	Sequence 2218 from Patent WO2068579.
ACCESSION	CQ716284
VERSION	CQ716284.1
KEYWORDS	GI:42277141
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1
AUTHORS	Venter, C.J., Adams M.C., Li, P.W. and Myers, E.W.
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL	Patent: WO 02068579-A 2218 06-SEP-2002; PE Corporation (NY) (US)
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		Query Match	81.9%	Score 455.2	DB 6	Length 1532					
		Best Local Similarity	88.7%	Pred. No. 1.6e-96							
		Matches 493	Conservative	0	Mismatches 63	Indels	0	Gaps	0		
QY	1	AAGAGCTCATGGGCGGTGGACAAGATGAGATCAGACGGCGGATGCCATCTTCGTG	60								
DB	453	AAGAGCTCATGGGCGCATGGAACAAGATGAGATCAGACACAGACGGCATCTTCGTC	512								
QY	61	CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCGCTACTTCTTCAGGCTGTTCGGAGCC	120								
DB	513	CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCGCCACTTCTTCAGGCTGTTCGGAGC	572								
QY	121	ACGGTCAAGCAGGTGGATTTTTTCAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG	180								
DB	573	ACGGTCAAGCAAGTGGACATTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG	632								

Qy	181	GTGAAGAGACACA	CAAAAGGCATGATCAATGACTTACTTTGGCCCAAGGGCTGTGGACCAG	240
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Qy	241	CTCACGGCTGGTTC	TGTGTAATGCCCTCTACTTCAACGGCCAGTGGAAGAAGCGCCCTTC	300
Dd	693	CTGACACGGCTGGTGT	GTAATGCCCCTCTACTTCAACGGCCAGTGGAAGACTCCCTTC	752
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Dd	873	TACTAGACATCTCT	GGAATCTGGCCTACCAAGGCAACACTCTGAGCATGTTTCAATTCGCGCC	932
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Dd	933	CCTATGAAAAAAG	AGGTGCTCTCTCGCGCCTCACCAGCAATTTCTGGACGCTCAGCTCATC	992
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RESULT 11

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HSPAIR1
LOCUS       Human mRNA for plasminogen activator inhibitor (PAI-1).
DEFINITION X04744
VERSION     X04744.1 GI:35275
KEYWORDS   glycoprotein; plasminogen activator inhibitor.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominiidae; Homo.
REFERENCE   1 (bases 1 to 1962)
AUTHORS     Wun,T.C. and Kretzmer,K.K.
TITLE       cDNA cloning and expression in E. coli of a plasminogen activator
            inhibitor (PAI) related to a PAI produced by Hep G2 hepatoma cell
JOURNAL     FEBS Lett. 210 (1), 11-16 (1987)
PUBMED     3026837
COMMENT     Data kindly reviewed (20-AUG-1987) by Wun T.-C.
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misc feature 645..647

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ORIGIN

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Best Local Similarity 88.7%; Pred. No. 1 6e-96;
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Qy 61 CAGGGGATCTGAGCTGCTCAGGCTTTCATGCCCTTCTTTCAGGCTGTTCCGGACC 120
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Qy 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGACGACGATTCATCATGATGACTGG 180
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Qy 361 CCCATGATGCTCAGACCAAGTTCACACTGAGTTTTCACCCCGCAGCGCCAT 420
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Db 679 TACTAGACATCTGGAATGCTTCCACGCGCAACACTTGAGCATGTTCAATGCGGCC 738
Qy 481 CCTTACGAAAGAGTGCTCTCTCGGCTTCCAGCAGATTCAGCAGCTGAGCTCATC 540
Db 739 CCTTACGAAAGAGTGCTCTCTCGGCTTCCAGCAGATTCAGCAGCTGAGCTCATC 798
Qy 541 AGCCAGTGGAAAGGGA 556
Db 799 AGCCAGTGGAAAGGGA 814

RESULT 12

BC010860
LOCUS
DEFINITION
Homo sapiens serine (or cysteine) proteinase inhibitor, clade E
(nexin, plasminogen activator inhibitor type 1), member 1, mRNA
(cDNA clone MGC:9226 IMAGE:3893914), complete cds.
ACCESSION
BC010860
VERSION
BC010860.1 GI:14790035
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 2207)
Straussberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketterman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2207)
NIH MGC Project
Direct Submission
Submitted (12-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 14 Row: 9 Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 10835158.

FEATURES

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SEQUENCE            CC413075      2660 bp     DNA
DEFINITION         Sequence 20146 from Patent WO0170979.
ACCESSION          CC413075
VERSION             CC413075.1   GI:41320856
KEYWORDS
SOURCE              Homo sapiens (human)
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE           1
AUTHORS             Lee,J. and Lillie,J.
TITLE               Genes, compositions, kits, and method for identification,
                    assessment, prevention, and therapy of ovarian cancer
JOURNAL             Patent: WO 0170979-A 20146 27-SEP-2001;
                    Millennium Pharmaceuticals, Inc. (US)
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QY 481 CCCTAGAAAAGAGGTGCCCTCTCTCCGCCCTCACCAGCATTTCTGGACGCTCAGCTCATC 540
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DEFINITION Sequence 10 from patent US 6103498.
ACCESSION AR106066
VERSION AR106066.1 GI:12820131
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2876)
AUTHORS Lawrence,D.A. and Stefansson,S.P.
TITLE Mutant plasminogen activator-inhibitor type 1 (PAI-1) and uses thereof
JOURNAL Patent: US 6103498-A 10 15-AUG-2000;
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Best Local Similarity 88.7%; Pred. No. 1.6e-96;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGGTGGAAACAAGATGAGATCAGACAGCGCGGATGCCATCTTTCGTG 60
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QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTTCAGGCTGTTCCGGACC 120
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Search completed: March 10, 2006, 01:01:12
Job time : 3290 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 22:55:30 ; Search time 471.5 Seconds

(without alignments)
7859.107 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: Geneseq2001as:*
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6: Geneseq2002as:*
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8: Geneseq2003as:*
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11: Geneseq2003ds:*
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13: Geneseq2004bs:*
14: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	456.4	82.1	2899	13 ADQ38428	AdQ38428 Human SNP
3	456.4	82.1	3320	13 ADQ38429	AdQ38429 Human SNP
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5	455.2	81.9	1209	10 AAD64654	Aad64654 Human pla
6	455.2	81.9	1209	14 ADV42563	Adv42563 Human psy
7	455.2	81.9	1209	14 AEA81050	Aea81050 Human pla
8	455.2	81.9	1962	10 ACF79499	AcF79499 Human pla
9	455.2	81.9	2016	13 ACN41744	Acn41744 Human dia
10	455.2	81.9	2053	13 ACN41743	Acn41743 Human dia
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12	455.2	81.9	2660	5 ADL61934	AdL61934 Human ova
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28	455.2	81.9	2876	14 AEB29660	Aeb29660 Human Ser
29	455.2	81.9	2937	13 ADR52878	Adr52878 Drug ther
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34	454.8	81.8	2876	10 ADE48114	AdE48114 Human PAI
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36	453.6	81.6	1482	10 AAD56136	Aad56136 Human pla
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38	452	81.3	2970	10 ACF79500	AcF79500 Mink plas
39	447.2	80.4	1187	12 ADM41307	Adm41307 Human pla
40	440.8	79.3	1482	1 AAN81524	Aan81524 Complete
41	420	75.5	3053	10 ACF79503	AcF79503 Rat plasm
42	420	75.5	3053	10 AAD64653	Aad64653 Rat plasm
43	420	75.5	3053	10 ABT41815	Abt41815 Toxicity
44	420	75.5	3053	11 ADW21854	Adw21854 Rat hepat
45	420	75.5	3053	12 ADP72654	Adp72654 Renal tox

ALIGNMENTS

RESULT 1

ACF79497

ID ACF79497 standard; cDNA; 2970 BP.

XX AC ACF79497;

XX AC ACF79497;

XX DT 18-DEC-2003 (first entry)

XX DE Cattle plasminogen activator inhibitor-1 cDNA.

XX KW Plasminogen activator inhibitor-1; PAI-1; cattle; transgenic;

XX KW thrombolytic; antiasthmatic; antiinflammatory; neutropic;

XX KW neuroprotective; antidepressant; nephrotropic; vulnary;

XX KW antiseborrheic; dermatological; antiarteriosclerotic; hepatotropic;

XX KW gene; ss.

XX OS Bos taurus.

XX XX

XX Key Location/Qualifiers

XX CDS 122..1330

XX FT /*tag= a

XX FT /product= "Cattle PAI-1"

XX XX

XX PN WO2003071267-A1.

XX XX

XX PD 28-AUG-2003.

XX XX

XX PF 19-FEB-2003; 2003WO-US005008.

XX XX

XX PR 19-FEB-2002; 2002US-0358061P.

XX XX

XX PA (UYVA-) UNIV VANDERBILT.

XX PA (DECL/) DECLERCK P J.

XX XX

XX PI Declerck PJ, Vaughan DE, Eren M;

XX XX

XX DR WPI; 2003-721694/68.

XX DR P-PSDB; ABR63122.

XX XX

XX PT Treating a warm-blooded vertebrate animal having a medical condition,

XX PT e.g. Alzheimer's disease, atherosclerosis, myelofibrosis or

XX PT glomerulosclerosis, comprises administering a plasminogen activator

Qy	61	CAGCGGGATCTGAAGCTGGTTCAGGGTTTCATGCGCTACTTCTTCAGGCTGTTCGGACC	120
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Qy	121	ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG	180
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Db	829	CTGACAGGCTGGTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC	888
Qy	301	CCAGAGAAAGCACTCACCAACGGGCTCTTCCACAAGTCTGATGGCAGCACCGTCTCTGTG	360
Db	889	CCCAGCTCCAGCACCCACCCACCGGCTCTTCCACAAATCAGAYGGCAGCACTGTCTCTGTG	948
Qy	361	CCCATGATGGCTCAGACCAACAAGTTCAACTACACTGAGTGTTCACCCCGCAGCGGCAT	420
Db	949	CCCATGATGGCTCAGACCAACAAGTTCAACTATCTGAGTTTCACCAACCGCGGATGGCCAT	1008
Qy	421	TACTACGACATCCTGGAAATGCCCTTACCAAGGCAACACTCTGAGCATGTTCATATGGCGCC	480
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XX	XX	AC	
XX	XX	ADQ38429;	
DT	DT	18-NOV-2004	(first entry)
XX	XX	DE	Human SNP containing myocardial infarction-associated gene, SEQ ID 92.
XX	XX	XX	Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX	XX	XX	cardiant; gene therapy; human; gene; ds.
OS	OS	Homo sapiens.	
XX	XX	WO2004058052-A2.	
PN	PN	15-JUL-2004.	
XX	XX	22-DEC-2003; 2003WO-US040978.	
XX	XX	20-DEC-2002; 2002US-0434778P.	
PR	PR	10-MAR-2003; 2003US-0453135P.	
PR	PR	30-APR-2003; 2003US-0466412P.	
PR	PR	23-SEP-2003; 2003US-0504955P.	
XX	XX	(APPL-) APPLERA CORP.	
PA	XX	Cargill M, Devlin JJ, Iakoubova O;	
PI	XX	WPI; 2004-533949/51.	
XX	XX	P-PSDB; ADQ39257.	
DR	DR	Identifying an individual who has an altered risk for developing	
XX	XX	PT myocardial infarction by detecting a single nucleotide polymorphism in	
PT	PT		

the individual's nucleic acids.

Claim 7; SEQ ID NO 92; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification and the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a human myocardial infarction-associated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 3320 BP; 825 A; 879 C; 828 G; 759 T; 0 U; 29 Other;

Query Match 82.1%; Score 456.4; DB 13; Length 3320;

Best Local Similarity 88.1%; Pred. No. 6.9e-111; Matches 490; Conservative 5; Mismatches 61; Indels 0; Gaps 0;

1	AGGAGCTCATGGGCGGTGGAA	CAAAGATGAGATCAGCACGGCCGATGCCATCTTCGTG	60
589	AAGGAGCTCAYGGGCGCATG	GAACAAGGAYGAGATCAGCACACAGACGCGRATCTTCGTC	648
61	CAGCGGATCTGAAGCTGGTCC	AGGGTTTCATGCCCTACTTCTTCAGGCTGTTCCGGACC	120
649	CAGCGGGATCTGAAGCTGGT	CCAGGCGTTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC	708
121	ACGGTCAAGCAGTGTGATTTT	TCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG	180
709	ACGGTCAAGCAAGTGACATT	TTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG	768
181	GTCAAGAGACACACAAAAGC	ATGATCAATGACTTACTTGGCCACAGGGGCTGTGGACCAG	240
769	GTGAAGACACACAAAAGTAT	GATCAGCAACTTGGTTGGGAAGGAGCCGTGGACCAG	828
241	CTGACGGCGCTGGTCTGTGG	TAATGCCCCTTACTTCAACGGCCAGTGGAAAACGCCCTTC	300
829	CTGACACGGCTGGTGTGGT	GAATGCCCTCTACTTCAACGGCCAGTGGGAAGACTCCCTTC	888
301	CCAGAGAAAGCACTCACAC	CGCCCTCTTCCACAAGTCTGATGGCAGCACCCTCTCTGTG	360
889	CCCGACTCCAGCACCCAC	CCGCCCTCTTCCAAAATCAGAYGGCAGCATGTCTCTGTG	948
361	CCCATGATGGCTCAGACCA	CAAGTTCAACTACACTGAGTTTTCACCCCCGACGCGCAT	420
949	CCCATGATGGCTCAGACCA	CAAGTTCAACTTACTGAGTTTCACACGCCCGATGGCCAT	1008
421	TACTACGACATCCTGGAA	TTCGCTTACCACGGCAACACTCTGAGCATGTTTCATTTGCGCC	480
1009	TACTACGACATCCTGGAA	CTGGCCCTACCAAGGGGACAMCCTCAGCATGTTTCATTTGCTGCC	1068
481	CCCTACGAAAAAGAGTG	CGCTCTCTCCGCCCTCACACAGCAATTCGACGCTCAGCTCATC	540
1069	CCTTATGAAAAAGAGTG	CGCTCTCTCTGCCCTCACCAACATTCCTGAGTGCCACAGCTCATC	1128

QY 541 AGCCAGTGGAAAGGGA 556
 Db 1129 AGCCACTGGAAAGGCA 1144

RESULT 4
 ADF28770
 ID ADF28770 standard; cDNA; 1209 BP.
 XX
 AC ADF28770;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human plasminogen-activator inhibitor-1 (PAI-1) encoding cDNA.
 XX
 KW Urokinase-type plasminogen activator; uPA;
 KW plasminogen-activator inhibitor-1; PAI-1; breast cancer; tumour;
 KW cancer therapy; human; ss; gene.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS
 FT 1. .1209
 FT /tag= a
 FT /product= "PAI-1"
 FT /note= "plasminogen activator inhibitor type 1"

WO2003082072-A2.
 XX
 XX 09-OCT-2003.
 XX
 XX 13-FEB-2003; 2003WO-US004538.
 XX
 XX 13-FEB-2002; 2002US-0356928P.
 PR
 PR 09-AUG-2002; 2002US-0402311P.
 XX
 XX (HARB/) HARBECK N.
 PA (KATE/) KATES R E.
 PA (SCHM/) SCHMITT M.
 PA (FOEK/) FOEKENS J A.
 XX
 XX Harbeck N, Kates RE, Schmitt M, Foekens JA;
 XX WPI; 2003-803930/75.
 DR P-PSDB; ADF28771.
 XX
 XX Selecting treatments for cancer, specifically breast cancer, based on
 PT levels of urokinase and plasminogen-activator inhibitor-1 in tissue.
 XX
 XX Disclosure; SEQ ID NO 3; 133pp; English.

The invention relates to selecting a treatment regime with highest expected benefit to a patient with primary breast cancer. The method involves measuring the levels of urokinase-type plasminogen activator (uPA) and plasminogen-activator inhibitor-1 (PAI-1), or corresponding mRNA, in primary tumour tissue (or a sample); and classifying the patient as low risk (LR) if the uPA level is below a cut-off value of between the 55 th . and 75 th percentile of normalized or analogous uPA in a randomized population of breast cancer patients, and if the PAI-1 level is lower than a cut-off value between the 61 st and 81 st percentile in the same population, or as high risk (HR) if the levels of uPA and PAI-1 are above these cut-off values. The treatment of LR (or HR) patients is then selected as one that results in the highest expected benefit in a comparable population of LR (or HR) patients. The method is used: for selection of the most effective therapy, including one designed to prevent relapse; and to predict expected benefit, overall or disease-free survival in patients with cancer, particularly of the breast but also leukemia and plasmacytoma. The method can also be used; to predict the benefit of preventative treatment for relapse of cancer, especially where HR patients are treated with bisphosphonate drugs; for deciding whether or not to administer an aggressive or non-aggressive regime; and for deciding whether or not to administer chemotherapy in combination with

CC hormone therapy (i.e. if the patient is LR, chemotherapy is not administered; in this case HR patients are those who are estrogen- and/or progesterone- receptor positive). The present sequence represents a cDNA encoding a human PAI-1 polypeptide.

XX
 SQ Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;
 Query Match 81.9%; Score 455.2; DB 10; Length 1209;
 Best Local Similarity 88.7%; Pred. No. 1e-110;
 Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAAGATGATGATCAGACGGCGATGCCATCTTCGTG 60
 Db 307 AAGGAGCTCATGGGCGCGTGGAAACAAAGATGATGATCAGACGGCGATCTTCGTG 366
 QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTTCAGGCTGTTCGGGACC 120
 Db 367 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTTCAGGCTGTTCGGGACC 426
 QY 121 ACGGTCAAGCAGAGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 180
 Db 427 ACGGTCAAGCAGAGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 486
 QY 181 GTGAAGACACACACAAAGGCGATGATCAATGATTTCTTGGCCAAAGGGCTGTGGACCCAG 240
 Db 487 GTGAAGACACACACAAAGGCGATGATCAATGATTTCTTGGGAAAGGAGCCGTGGACCCAG 546
 QY 241 CTGACGGCGCTGGTTCCTGGTGAATGCCCTCTACTTTCAGAGCGCCAGTGGAAAGCGCCCTTC 300
 Db 547 CTGACAGCGCTGGTGGTGAATGCCCTCTACTTTCAGAGCGCCAGTGGAAAGACTCCCTTC 606
 QY 301 CCAGAGAAAAGCAGCTCAGCACCGCCTCTTCCAAAGTCTGTATGGCAGACCCGCTCTCTGTG 360
 Db 607 CCGGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 666
 QY 361 CCCATGATGGCTCAGACCAACAAAGTTCACTACATGATTTTCACCCCGACGGCCAT 420
 Db 667 CCCATGATGGCTCAGACCAACAAAGTTCACTACATGATTTTCACCCCGACGGCCAT 726
 QY 421 TACTACGACATCTTGAATTCGCCCTTACCAGCGCACACTCTGAGCATGTTCATTCGCCGC 480
 Db 727 TACTACGACATCTTGAATTCGCCCTTACCAGCGCGACACCTCAGCATGTTCATTCGCCGC 786
 QY 481 CCCTACGAAAAGAGGTGCCTCTCTCCGCCCTCACCAGCATTTCTGGAGCTCAGCTCATC 540
 Db 787 CCTATGAAAAGAGGTGCCTCTCTCTGCCCTCACCAGCATTTCTGAGTGGCCAGCTCATC 846
 QY 541 AGCCAGTGGAAAGGGA 556
 Db 847 AGCCACTGGAAAGGCA 862

RESULT 5
 AAD64654
 ID AAD64654 standard; cDNA; 1209 BP.
 XX
 AC AAD64654;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human plasminogen activator inhibitor-1 (PAI-1) coding region.
 XX
 KW Plasminogen activator inhibitor-1; PAI-1; cardiovascular disease;
 KW fibrotic disease; gene therapy; antiinflammatory; gene; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS
 FT 1. .1209
 FT /tag= a
 FT /product= "Human plasminogen activator inhibitor-1 protein"
 FT /note= "Capital T represents cleavage sites"

XX US2003199463-A1.
XX 23-OCT-2003.
XX 23-APR-2002; 2002US-00128706.
XX 23-APR-2002; 2002US-00128706.
XX (ITES/) ITESCU S.
XX Itescu S;
XX WPI; 2003-852809/79.
XX P-PSDB; ABW02690.
XX New catalytic nucleic acid that hybridizes to and specifically cleaves an
PT mRNA encoding a Plasminogen Activator Inhibitor-1, useful in preparing a
PT composition for treating e.g., cardiovascular or fibrotic disease.
XX Disclosure; SEQ ID NO 17; Opp; English.
XX The present invention relates to a new catalytic nucleic acid that
CC hybridizes to and specifically cleaves an mRNA encoding a plasminogen
CC activator inhibitor-1 (PAI-1). The invention is useful in preparing a
CC composition for treating cardiovascular or fibrotic disease. The
CC invention is also used in gene therapy. The present sequence is human
CC plasminogen activator inhibitor-1 (PAI-1) coding region
XX
SQ Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 10; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 60
DB 307 AAGGAGCTCATGGGCGCGTGGAAACAAGATGAGATCAGACGCGCGATCTTCGTG 366
QY 61 CAGCGGATCTGAAGTGTGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAGCC 120
DB 367 CAGCGGATCTGAAGTGTGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAGC 426
QY 121 ACGGTCAAGCAGTGATTTTCAGATGAGCAGACGCGCGATTCATCATCAATGACTG 180
DB 427 ACGGTCAAGCAGTGATTTTCAGATGAGCAGACGCGCGATTCATCATCAATGACTG 486
QY 181 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCACGCGGTGTGGACCA 240
DB 487 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCACGCGGTGTGGACCA 546
QY 241 CTGACGCGCTGTGTTCTGTGTAATGCCCTTCTTCAACGCGCGATGGAAAGCGCCCTTC 300
DB 547 CTGACGCGCTGTGTTCTGTGTAATGCCCTTCTTCAACGCGCGATGGAAAGCATCTCCCTTC 606
QY 301 CCAGAGAAAGCACTCACCACGCGCTTTCACCAAGTCTGATGCGAGCACCGTCTCTGTG 360
DB 607 CCGGACTCCAGCACCCACGCGCGCTTTCACCAAGTCTGATGCGAGCACCGTCTCTGTG 666
QY 361 CCATGATGGCTCAGACACCAAGTTCAACTACACTGAGTTTTCACCCCGGACGCGCAT 420
DB 667 CCATGATGGCTCAGACACCAAGTTCAACTACACTGAGTTTTCACCCCGGACGCGCAT 726
QY 421 TACTACGACATCTGGAATTGCCCTTACCACGCGCAACACTCTGAGCATGTTTCATGCGGCC 480
DB 727 TACTACGACATCTGGAATTGCCCTTACCACGCGCAACACTCTGAGCATGTTTCATGCGGCC 786
QY 481 CCTTACGAAAAGAGTGCTCTCTCCGCGCTTTCACGACATTCGACGCTCAGCTCATC 540
DB 787 CCTTATGAAAAGAGTGCTCTCTCTGCGCTTTCACCAACATTCGAGTCCCGAGCTCATC 846
QY 541 AGCCATGTGAAGGGA 556

DB 847 AGCCACTGGGAAGGCA 862
RESULT 6
ADV42563
ID ADV42563 standard; cDNA; 1209 BP.
XX AC ADV42563.
XX 10-MAR-2005 (first entry)
XX Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 191.
XX microarray; psychoneuroendocrinimmune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX Homo sapiens.
XX WO2004108899-A2.
XX 16-DEC-2004.
XX 04-JUN-2004; 2004WO-US017686.
XX 04-JUN-2003; 2003US-0475915P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Nicholson A, Vernon SD;
XX WPI; 2005-031682/03.
XX New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX Claim 1; SEQ ID NO 191; 254pp; English.
XX The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specification mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX
SQ Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 14; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 60
DB 307 AAGGAGCTCATGGGCGCGTGGAAACAAGATGAGATCAGACGCGCGATCTTCGTG 366
QY 61 CAGCGGATCTGAAGTGTGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAGCC 120
DB 367 CAGCGGATCTGAAGTGTGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAGC 426
QY 121 ACGGTCAAGCAGTGATTTTCAGATGAGCAGACGCGCGATTCATCATCAATGACTG 180
DB 427 ACGGTCAAGCAGTGATTTTCAGATGAGCAGACGCGCGATTCATCATCAATGACTG 486
QY 181 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCACGCGGTGTGGACCA 240
DB 487 GTGAAGAGACACACAAAAGCATGATCAATGACTTACTTGGCCACGCGGTGTGGACCA 546
QY 241 CTGACGCGCTGTGTTCTGTGTAATGCCCTTCTTCAACGCGCGATGGAAAGCGCCCTTC 300

Db 547 CTGACACGGCTGGTGTGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 606
QY 301 CCAGAGAAAAGCACTCACCACCGCCTCTTCCACAAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 607 CCGGACTCCAGCACCCACCGCGCCTCTTCCAAATCAGACGGCAGCACTGTCTGTG 666
QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACTAGTTTTCACCCCGACGCCAT 420
Db 667 CCATGATGGCTCAGACCAACAAAGTTCAACTACTAGTTTTCACCCCGACGCCAT 726
QY 421 TACTAGGACATCTGGAATTCCTTACACGGCAGCACTCTGAGCATGTTCAATTCGCC 480
Db 727 TACTAGGACATCTGGAATTCCTTACACGGCAGCACTCTGAGCATGTTCAATTCGCC 786
QY 481 CCTACGAAAAGAGTGCTCTCTCCGCCCTCACCAGCATTTCTGACGCTCAGTCTCATC 540
Db 787 CTTATGAAAAGAGTGCTCTCTCTGCCCTCACCAGCATTTCTGAGTGCCAGTCTCATC 846
QY 541 AGCCAGTGAAGGGA 556
Db 847 AGCCACTGGAAGGCA 862

RESULT 7
AEA81050
ID AEA81050 standard; cDNA; 1209 BP.
AC AEA81050;
XX
DT 08-SEP-2005 (first entry)
XX
DE Human plasminogen activator inhibitor-1 encoding cDNA SEQ ID NO:17.
XX
KW antisense therapy; RNA interference; plasminogen activator inhibitor-1;
KW vasotrophic; thrombolytic; hemostatic; vascular disease;
KW thrombocyte disorder; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..1209
FT /*tag= a
FT /product= "plasminogen activator inhibitor-1 (PAI-1)"
XX
XX US2005148527-A1.
XX
XX 07-JUL-2005.
XX
XX 24-FEB-2005; 2005US-00512496.
XX
XX 23-APR-2002; 2002US-00128706.
XX
XX 23-APR-2003; 2003WO-US012767.
XX
XX (ITES/) ITESCU S.
XX
XX Itescu S;
XX
XX WPI: 2005-478099/48.
XX
XX P-PSDB; AEA81039.
XX

New catalytic nucleic acid that specifically cleaves an mRNA encoding a plasminogen activator inhibitor-1 (PAI-1), useful for treating vascular, thrombotic or hemostatic disorders.

Disclosure; SEQ ID NO 17; 53pp; English.

XX
XX The invention relates to a catalytic nucleic acid that specifically
XX cleaves an mRNA encoding a plasminogen activator inhibitor-1 (PAI-1).
XX Also described: (1) a pharmaceutical composition comprising the catalytic
XX nucleic acid, oligonucleotide, or inhibitor of PAI-1 expression, and a
XX carrier; (2) a method of treating a cardiovascular disease in a subject;
XX (3) a method of treating a vascular disease in a subject where the
XX disease is treated by reducing thrombin or fibrin production; (4) a

CC method of treating a vascular disease in a subject where the vascular
CC disease is treated by inhibition of PAI-1 expression; (5) a method of
CC inducing neovascularization in a heart tissue of a subject; (6) a method
CC of inhibiting smooth muscle cell proliferation in a tissue of a subject;
CC (7) a method of inhibiting thrombin and fibrin deposition in a heart or
CC tissue of a subject; (8) a method of treating a subject suffering from a
CC thrombotic disease or disorder, or hemostatic disorder where the disease
CC or disorder is associated with elevated expression of PAI-1; and (9) a
CC method of treating a disorder of a subject's heart involving loss of
CC cardiomyocytes. The nucleic acid, compositions and methods are useful for
CC treating vascular, thrombotic or hemostatic disorders. The present
CC sequence encodes human PAI-1, which is used in the exemplification of the
CC present invention.
XX

SQ Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;

Query Match 81.9%; Score 455.2; DB 14; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCTGGAAACAAAGATGAGATCAGACGGCGGATGCCATCTTCGTG 60
Db 307 AAGGAGCTCATGGGCGCATGGAAACAAAGATGAGATCAGACGGCGGATCTTCGTG 366
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGACC 120
Db 367 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGAGC 426
QY 121 ACGGTCAAGCAGGTGGATTTTCAGAGATGACAGAGCAGGTTTCATCATCAATGACTGG 180
Db 427 ACGGTCAAGCAGGTGGACTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 486
QY 181 GTGAAGACACACACAAAGGATGATCAATCACTTTACCTTGGCCAAAGGGCTGTGACACAG 240
Db 487 GTGAAGACACACACAAAGGATGATCAATCACTTTACCTTGGCCAAAGGGCTGTGACACAG 546
QY 241 CTGACGCGCTGGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAACGCCCTTC 300
Db 547 CTGACACGGCTGGTGTGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606
QY 301 CCAGAAAAGCACTCACCACCGCCTCTTCCACAAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 607 CCGGACTCCAGCACCCACCGCGCCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 666
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGTAGTTTTCACCCCGACGCCCAT 420
Db 667 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGTAGTTTTCACCCCGACGCCCAT 726
QY 421 TACTACGACATCTTGGAAATTCCTTACACGGCCAACTCTGAGCATGTTTCATTCGCCCC 480
Db 727 TACTACGACATCTTGGAAATTCCTTACACGGCCAACTCTGAGCATGTTTCATTCGCCCC 786
QY 481 CCCTACGAAAAGAGTGCTCTCTCCGCCCTCACCAGCATTTCTGAGCGCTCAGTCTCATC 540
Db 787 CTTATGAAAAGAGTGCTCTCTCTCGCCCTCACCACATTTCTGAGTGGCCAGCTCATC 846
QY 541 AGCCAGTGAAGGGA 556
Db 847 AGCCACTGGAAGGCA 862

RESULT 8
ACF79499
ID ACF79499 standard; cDNA; 1962 BP.
XX
XX ACF79499;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human plasminogen activator inhibitor-1 partial cDNA.
XX
XX Plasminogen activator inhibitor-1; PAI-1; human; transgenic;
XX thrombolytic; antithrombotic; antiinflammatory; nootropic;
XX

KW neuroprotective; antidepressant; nephrotropic; vulnery;
KW antiseborrheic; dermatological; antiarteriosclerotic; hepatotropic;
KW gene; ss.
OS Homo sapiens.
XX
FH Location/Qualifiers
FT 1. .1161
FT /tag= a
FT /partial
FT /product= "Human PAI-1"
FT /note= "No start codon"
XX
XX WO2003071267-A1.
XX
XX 28-AUG-2003.
XX
XX 19-FEB-2003; 2003WO-US0005008.
XX
XX 19-FEB-2002; 2002US-0358061P.
XX (UYVA-) UNIV VANDERBILT.
XX (DECL/) DECLERCK P J.
XX Declerck PJ, Vaughan DE, Eren M;
XX WPI: 2003-721694/68.
XX P-PSDB; ABR63124.
XX
XX Treating a warm-blooded vertebrate animal having a medical condition,
PT e.g. Alzheimer's disease, atherosclerosis, myelofibrosis or
PT glomerulosclerosis, comprises administering a plasminogen activator
PT inhibitor-1 inhibitor.
XX
PS Disclosure; Page 64-66; 91pp; English.
XX
CC The present sequence is that a partial cDNA for human plasminogen
CC activator inhibitor-1 (PAI-1). The PAI-1 gene can be used to produce
CC transgenic animals of the invention, useful for screening potential PAI-1
CC inhibitors. Such PAI-1 inhibitors can be used to treat a warm-blooded
CC vertebrate animal having a medical condition, e.g. alopecia, undesired
CC weight loss, Alzheimer's disease, systemic amyloidosis, myelofibrosis,
CC glomerulosclerosis, male pattern baldness, keloids, apocrine cysts, acne,
CC atherosclerosis, ageing, or a wound (claimed). A method of testing a
CC candidate composition for PAI-1 inhibition activity comprises
CC administering the composition to a transgenic animal having a PAI-1 gene
CC incorporated into its genome, and observing an ameliorating change in the
CC animal indicative of inhibition of PAI-1 activity, the change being an
CC improvement of a vascular thrombotic disorder, asthma, chronic
CC obstructive pulmonary disease, alopecia, undesired weight loss such as
CC anorexia, Alzheimer's disease, systemic amyloid deposition, systemic
CC amyloidosis, myelofibrosis, glomerulosclerosis, male pattern baldness,
CC keloids, apocrine cysts, acne, atherosclerosis, ageing,
CC hepatosplenomegaly, extramedullary haematopoiesis, or a wound (claimed)
XX
SQ Sequence 1962 BP; 456 A; 569 C; 505 G; 432 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 10; Length 1962;
Best Local Similarity 88.7%; Pred. No. 1.2e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGGTGGACAAAGATGAGATCAGACGCGCGATCCCATCTTCGGT 60
DB 259 AAGGAGCTCATGGGCGGTGGACAAAGATGAGATCAGACGCGCGATCTTCGTC 318
QY 61 CAGCGGATCTGAAGCTGTTCAGGGTTCATGCCCTTCTTCAGGCTGTTCGGAC 120
DB 319 CAGCGGATCTGAAGCTGTTCAGGGTTCATGCCCTTCTTCAGGCTGTTCGGAGC 378
QY 121 ACGGTCAAGCAGGTGATTTTTCAGAGATGGACAGAGCAGGTTCATCATCAATCACTGG 180
DB 379 ACGGTCAAGCAGGTGATTTTTCAGAGATGGACAGAGCAGGTTCATCATCAATCACTGG 438

QY 181 GTCAAGAGACACACAAAAGGCATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACAG 240
DB 439 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCGGTGGACAG 498
QY 241 CTGACGCGCTGTTCTTGGTGAATGCGCTTACTTCAACGCGCAGTGGAAGAAAGCGCCCTTC 300
DB 499 CTGACACGGCTGGTGTGGTGAATGCGCTTACTTCAACGCGCAGTGGAAGACTCCCTTC 558
QY 301 CCAGAGAAAAGCACTCACCACCGCCTCTTCCCAAAGTCTGATGGCAGCACCGTCTCTGTG 360
DB 559 CCGGACTCCAGCACCCACCGCGCTCTTCCCAAATCAGACGGCAGCACTGCTCTGTG 618
QY 361 CCCATGATGCTCAGACCAACCAAGTTCAACTACACTGAGTTTCCACCCCGAGGCGCAT 420
DB 619 CCCATGATGCTCAGACCAACCAAGTTCAACTACACTGAGTTTCCACCGCGGATGGCCAT 678
QY 421 TACTACGACATCTCGGAATTGCGCTACCAACGCGCAACTCTGAGCATGTTTCATTTGCCGCC 480
DB 679 TACTACGACATCTCGGAATTGCGCTACCAACGCGGACACCTCAGCATGTTTCATTTGCCGCC 738
QY 481 CCCTACGAAAAGAGTGGCTCTCTCCGCCCTCACCAGCATTTCTGGACGCTCAGCTCATC 540
DB 739 CCTTATGAAAAGAGTGGCTCTCTCGCCCTCACCACCAATTTCTGAGTGCCGAGTCTATC 798
QY 541 AGCCAGTGGAAAGGA 556
DB 799 AGCCACTGGAAAGGCA 814
RESULT 9
ACN41744
ID ACN41744 standard; cDNA; 2016 BP.
XX
XX ACN41744;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human diagnostic and therapeutic polynucleotide SEQ ID NO:619.
DE ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KW dithp.
XX
XX Homo sapiens.
XX
XX WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
XX 12-SEP-2003; 2003WO-US028227.
XX
XX 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
XX
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patry S, Shi X, Suarez CJ;
XX
XX WPI: 2004-329368/30.
XX
XX P-PSDB; ABR83092.
DR
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 1; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 2016 BP; 464 A; 628 C; 508 G; 416 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 13; Length 2016;
Best Local Similarity 88.7%; Pred. No. 1.2e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCTGGGAACAAAGATGAGATCAGCAGCGCGCATGCCATCTTCGTG 60
Db |||||
QY 61 CAGCGGGATCTGAAGCTGGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGACC 120
Db |||||
QY 489 CAGCGGGATCTGAAGCTGGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAGC 548
Db |||||
QY 121 ACGGTCACAGCAGTGATTTTCAGAGATGGACAGCGAGTTTCATCATCAATCACTGG 180
Db |||||
QY 549 ACGGTCACAGCAGTGATTTTCAGAGATGGAGAGCGAGTTTCATCATCAATCACTGG 608
Db |||||
QY 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTTGGCAAGGGCTGTGGACCA 240
Db |||||
QY 609 GTGAAGAGACACACAAAAGGATGATCAGCACTTGTCTGGAAAGAGCGGTGGACCA 668
QY 241 CTGACGGCTGTGTTCTGGTAATGCCCTTACTTCAACGGCCAGTGAAACGCCCTTC 300
Db |||||
QY 669 CTGACAGCGCTGTGTTCTGGTAATGCCCTTACTTCAACGGCCAGTGAAAGACTCCCTTC 728
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCACAAGTCTGATGGCAGCACCGTCTCTGTG 360
Db |||||
QY 729 CCGGACTCAGCACCACCGCGCTCTTCCACAATCAGAGCGGAGCACTGTCTCTGTG 788
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACCCCGACGCCAT 420
Db |||||
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QY 421 TACTACGACATCCTGGAAATGGCCCTTACACGGCAACACTCTGAGCATGTTTCAATTCGCGC 480
Db |||||
QY 849 TACTACGACATCCTGGAAATGGCCCTTACACGGGACACCTCAGCATGTTTCAATTCGCGC 908
QY 481 CCTACGAAAGAGGTGCTCTCTCCGCCCTCACCAGCATCTCGAGCTCAGTCTATC 540
Db |||||
QY 909 CTTTATGAAAGAGGTGCTCTCTCTGCGCTTCCACAAATCTCTGAGTGCCCGATCTATC 968
QY 541 AGCCAGTGGAAAGGGA 556
Db |||||
QY 969 AGCCACTGGAAGGCA 984
RESULT 10
ID ACN41743
ID ACN41743 standard; cDNA; 2053 BP.
XX ACN41743;
AC ACN41743;
XX 18-NOV-2004 (first entry)
XX

DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:618.
XX ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KW dithp.
XX Homo sapiens.
XX WO2004023973-A2.
XX 25-MAR-2004.
XX 12-SEP-2003; 2003WO-US028227.
XX 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Eldred LV;
PI Mooney EM, Deleageane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EU, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
DR P-FSDB; ABW83091.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 1; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 2053 BP; 471 A; 642 C; 512 G; 428 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 13; Length 2053;
Best Local Similarity 88.7%; Pred. No. 1.2e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCTGGGAACAAAGATGAGATCAGCAGCGCGCATGCCATCTTCGTG 60
Db |||||
QY 61 CAGCGGGATCTGAAGCTGGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGACC 120
Db |||||
QY 526 CAGCGGGATCTGAAGCTGGTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGAGC 585
QY 121 ACGGTCACAGCAGTGATTTTCAGAGATGGACAGCGAGTTTCATCATCAATCACTGG 180
Db |||||
QY 586 ACGGTCACAGCAGTGATTTTCAGAGATGGAGAGCGAGTTTCATCATCAATCACTGG 645
QY 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTTGGCAAGGGCTGTGGACCA 240

PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 20146; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.
XX
SQ Sequence 2660 BP; 615 A; 799 C; 653 G; 593 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 5; Length 2660;
Best Local Similarity 88.7%; Pred. No. 1.3e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGGTGGGAACAAAGATGATGATCAGCAGCGCGGATCCATCTCTG 60
DB 452 AAGGAGCTCATGGGCGGTGGGAACAAAGATGATGATCAGCAGCGCGGATCTCTGTC 511
QY 61 CAGCGGGATCTCAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 120
DB 512 CAGCGGGATCTCAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 571
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGCAGGTTTCATCATCAATCACTGG 180
DB 572 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGGTTTCATCATCAATCACTGG 631
QY 181 GTGAGAGACACACAAAGGATGATCAATGATCTTACTTGGCCAGGGCTGTGACCCAG 240
DB 632 GTGAGAGACACACAAAGGATGATCAATGATCTTACTTGGCCAGGGCTGTGACCCAG 691
QY 241 CTGACGCGCGCTGGTCTGGTGAATGCTCTACTTCAACGCGCAGTGGGAAAACGCGCTTC 300

DB 692 CTGACACGCTGGTGGTGAATGCCCTTACTTCAACGCGCAGTGGGAAGACTCCCTTC 751
QY 301 CCAGAGAAAAGCACTCACCACCGGCTCTTCCAAAGTCTGATGGCAGCACCCTCTCTGTG 360
DB 752 CCCGACTCCAGCACCACCGGCTCTTCCAAAGTCTGATGGCAGCACCCTCTCTGTG 811
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACCCCGCAGCGCCAT 420
DB 812 CCCATGATGGCTCAGACCAACAAAGTTCAACTATATCTAGTTTCCACACCGCGGATGGCCAT 871
QY 421 TACTACGACATCTCTGGAATTCCTTACCAAGCAACTCTGAGCATGTTTCAATTCGCGCC 480
DB 872 TACTACGACATCTCTGGAATTCCTTACCAAGCAACTCTGAGCATGTTTCAATTCGCGCC 931
QY 481 CCCTACGAAAAGAGGTGCTCTCTCCGCGCTCACCAGCATCTCGAGCGCTCAGCTCATC 540
DB 932 CTTTATGAAAAGAGGTGCTCTCTCTGCGCTCACCACAAATCTGAGTCCCGCAGTCTATC 991
QY 541 AGCCAGTGGAAAGGGA 556
DB 992 AGCCACTGGAAAGGCA 1007
RESULT 13
ID ABV94750 standard; cDNA; 2870 BP.
XX AC ABV94750;
XX DT 14-JAN-2003 (first entry)
DE Human pancreatic cancer expressed cDNA SEQ ID NO 131.
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
XX OS Homo sapiens.
XX PN WO200260317-A2.
XX PD 08-AUG-2002.
XX PF 30-JAN-2002; 2002WO-US002781.
XX PR 30-JAN-2001; 2001US-0265305P.
XX PR 31-JAN-2001; 2001US-0265682P.
XX PR 09-FEB-2001; 2001US-0267568P.
XX PR 21-MAR-2001; 2001US-0278651P.
XX PR 28-APR-2001; 2001US-0287112P.
XX PR 16-MAY-2001; 2001US-0291631P.
XX PR 12-JUL-2001; 2001US-0305484P.
XX PR 20-AUG-2001; 2001US-0313999P.
XX PR 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
XX P-PSDB; ABP68605.
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
XX Claim 1; SEQ ID NO 131; 300pp + Sequence Listing; English.
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV94645); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity

to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-ABP68637) encoded by (1) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 2870 BP; 704 A; 792 C; 725 G; 649 T; 0 U; 0 Other;

Query Match. 81.9%; Score 455.2; DB 6; Length 2870;
Best Local Similarity 88.7%; Pred. No. 1.4e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60
Db 376 AAGGAGCTCATGGGCGGTGGACAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGCGAAC 120
Db 436 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGCGAAC 120
QY 121 ACGGTCAGGAGTGGATTTTTCAGAGATGGAGAGCCAGGTTTCATCATCAATGACTGG 180
Db 496 ACGGTCAGGAGTGGATTTTTCAGAGATGGAGAGCCAGGTTTCATCATCAATGACTGG 180
QY 181 GTGAGAGACACACAAAGGATGATCAATGACTTCTTGGCCAGGGGCTGTGGACGAG 240
Db 556 GTGAGAGACACACAAAGGATGATCAATGACTTCTTGGCCAGGGGCTGTGGACGAG 240
QY 241 CTGACGCGCTGTGTGGTGAATGCCCTCTACTTCAACGCGCAGTGGAAGACGCCCTTC 300
Db 616 CTGACGCGCTGTGTGGTGAATGCCCTCTACTTCAACGCGCAGTGGAAGACGCCCTTC 300
QY 301 CCAGAGAAAGACTCACACCGGCTTCTCCAAAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 676 CCGGACTCCAGCACCGGCTTCTCCAAAGTCTGATGGCAGCACCGTCTCTGTG 360
QY 361 CCCATGATGCTCAGACCAAGATTTCACTAAGTGTTCACCCCGGAGGCGCAT 420
Db 736 CCCATGATGCTCAGACCAAGATTTCACTAAGTGTTCACCCCGGAGGCGCAT 420
QY 421 TACTACGACATCTGGAATTTGCCCTTACCGGCAACTCTGAGCATGTTCATTCGCGCC 480
Db 796 TACTACGACATCTGGAATTTGCCCTTACCGGCAACTCTGAGCATGTTCATTCGCGCC 480
QY 481 CCCTACGAAAGAGGTGCTCTCTCGGCGCTCACCAGCAATTCGACGCTCAGCTCATC 540
Db 856 CCCTATGAAAGAGGTGCTCTCTCGGCGCTCACCAGCAATTCGACGCTCAGCTCATC 540
QY 541 AGCCAGTGGAAAGGGA 556
Db 916 AGCCACTGGAAAGGCA 931

RESULT 14

AAT97303
ID AAT97303 standard; DNA; 2876 BP.

XX
AC
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XX
XX
DT 14-APR-1998 (first entry)

XX Human plasminogen activator inhibitor DNA.

XX Plasminogen activator inhibitor type 1; PAI-1; human; elastase inhibitor;

XX vitronectin; cell attachment; cell migration; cell proliferation;

XX emphysema; adult respiratory distress syndrome; acute lung inflammation;

XX

KW alpha 1-antitrypsin deficiency; cystic fibrosis; atopic dermatitis;
KW pancreatitis; periodontal disease; arthritis; HIV; atherosclerosis;
KW restenosis; neointima; fibrosis; wound healing; tumour; metastasis;
KW psoriasis; thrombosis; angiogenesis; therapy; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

PH CDS 76..1284

FT sig_peptide /*tag= a

FT mat_peptide /*tag= b

FT mat_peptide 145..1281

FT /*tag= c

XX WO9739028-A1.

XX 23-OCT-1997.

XX 11-APR-1997; 97WO-US006071.

XX 12-APR-1996; 96US-0015299P.

XX (AMNA-) AMERICAN NAT RED CROSS.

XX Lawrence DA, Stefansson SP;

XX WPI; 1997-526399/48.

XX P-PSDB; AAW31587.

XX Plasminogen activator-inhibitor type I mutant inhibits elastase - or has

XX high affinity for vitronectin, for therapeutic inhibition of elastase or

XX vitronectin-mediated cell attachment, migration etc.

XX Disclosure; Page 91-95; 144pp; English.

XX This nucleotide sequence codes for wild-type human plasminogen activator

XX inhibitor type (PAI-1) (see AAW31587). Novel mutants (see AAW26710-25) of

XX the PAI-1 mature protein are claimed that inhibit elastase or other

XX elastase-like proteases, or are inhibitors of vitronectin-dependent cell

XX migration. The mutants are obtained by site-directed mutagenesis of the

XX PAI-1 DNA sequence and expression in host cells, and have a range of

XX therapeutic uses

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QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACACCCCGACGGCCAT 420
Db 742 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACACCGCCGATGGCCAT 801
QY 421 TACTAGGACATCTGGAAATTCCTTACCAACGGCAACACTCTGAGCATGTTTCATTCGCGCC 480
Db 802 TACTAGGACATCTGGAAATTCCTTACCAACGGCAACACTCTGAGCATGTTTCATTCGCGCC 861
QY 481 CCTTACGAAAAGAGTGCTCTCTCGGCCCTCACCAGCATTTCTGGACGCTCAGCTCATC 540
Db 862 CCTTATGAAAAGAGTGCTCTCTCGGCCCTCACCAGCATTTCTGAGTGCCAGCTCATC 921
QY 541 AGCCAGTGGAAAGGGA 556
Db 922 AGCCACTGGAAAGGCA 937
RESULT 15
AAS09460
ID AAS09460 standard; cDNA; 2876 BP.
XX
AC AAS09460;
XX
DT 26-SEP-2001 (first entry)
XX
DE Human cDNA encoding Plasminogen activator inhibitor-1, PAI-1.
XX
KW Human; Plasminogen activator inhibitor-1; PAI-1; serpin;
KW immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome;
KW ARDS; HIV infection; Human immunodeficiency virus; prostate cancer;
KW TNF-mediated inflammation; benign prostatic hypertrophy; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT 76..1284
FT /*tag= a
FT /product= "PAI-1"
FT 76..143
FT /*tag= c
FT /note= "Alternative signal peptide"
FT 76..138
FT /*tag= b
FT /note= "Alternative signal peptide"
FT 139..1281
FT /*tag= d
FT /label= Mature_PAI_1 #1
FT /note= "Both forms of the protein are detected in vivo"
FT 144..1281
FT /*tag= e
FT /label= Mature_PAI_1 #2
FT /note= "Both forms of the protein are detected in vivo"
XX
PN WO200138560-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032315.
XX
PR 22-NOV-1999; 99US-0167553P.
XX
PA (AMNA-) AMERICAN NAT RED CROSS.
XX
PI Lawrence DA, Day D;
XX
DR WPI; 2001-441438/47.
XX P-PSDB; AAU04913.
XX
PT Detecting a functionally active form of an enzyme in a biological sample
PT comprises contacting an enzyme inhibitor immobilized on a solid
XX substrate.
XX

PS Disclosure; Fig 3; 69pp; English.
XX
CC The sequence encodes human plasminogen activator inhibitor-1, PAI-1, a
CC serine proteinase inhibitor or serpin. The protein is used to demonstrate
CC the method of the invention which comprises detecting a functionally
CC active form of an enzyme in a biological sample by contacting an enzyme
CC inhibitor immobilised on a solid substrate with the biological sample and
CC measuring the binding of the enzyme inhibitor to the active form of the
CC enzyme by a detectable label, where the enzyme inhibitor specifically
CC forms a covalent bond or binds with a dissociation constant of 1 x 10⁻⁹M
CC or less with the active form of the enzyme. The present invention
CC provides a sensitive method for the detection of a functionally active
CC form of an enzyme in a biological sample. Human PAI-1 can be used to
CC detect a number of enzymes including tissue plasminogen activator,
CC urokinase, thrombin, plasmin, neutrophil elastase, pancreatic elastase,
CC trypsin, chymotrypsin, cathepsin G and prostate specific antigen and as
CC such can be used in methods to diagnose diseases such as cystic fibrosis,
CC acute respiratory distress syndrome (ARDS), HIV infection, TNF-mediated
CC inflammation, prostate cancer and benign prostatic hypertrophy
XX
SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;
Query Match 81.9%; Score 455.2; DB 4; Length 2876;
Best Local Similarity 88.7%; Fred. No. 1.4e-110;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGGCCGTGGAAACAAAGATGAGATCAGACGCGCGATGCCATCTTCGTG 60
Db 382 AAGGAGCTCATGGGGCCATGGAAACAAAGATGAGATCAGACGCGCGATCTTCGTG 441
QY 61 CAGCGGGAATGGAAGCTGGTTCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGGACC 120
Db 442 CAGCGGGAATGGAAGCTGGTTCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGGAGC 501
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGTGCAGACGCGAGCTTCATCATCAATCACTGG 180
Db 502 ACGGTCAAGCAGGTGGATTTTTCAGAGTGCAGAGAGAGCCAGATTCATCAATCACTGG 561
QY 181 GTGAAGAGACACACAAAAGGCATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCAAG 240
Db 562 GTGAAGAGACACACAAAAGGCATGATCAAGCAACTTGTGGAAAGGAGCGGTGGACCAAG 621
QY 241 CTGACGCGCTGGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAACACGCCCTTC 300
Db 622 CTGACGCGCTGGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAGACTCCCTTC 681
QY 301 CCAGAGAAAAGCACTACACACCGGCTCTTCACAAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 682 CCCGACTCCAGCACCCACCGCGGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 741
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACACCCCGACGGCCAT 420
Db 742 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACACCGCCGATGGCCAT 801
QY 421 TACTACGACATCTGGAAATTCCTTACCAACGGCAACACTCTGAGCATGTTTCATTCGCGCC 480
Db 802 TACTACGACATCTGGAAATTCCTTACCAACGGCAACACTCTGAGCATGTTTCATTCGCGCC 861
QY 481 CCTTACGAAAAGAGTGCTCTCTCGGCCCTCACCAGCATTTCTGGACGCTCAGCTCATC 540
Db 862 CCTTATGAAAAGAGTGCTCTCTCGGCCCTCACCAGCATTTCTGAGTGCCAGCTCATC 921
QY 541 AGCCAGTGGAAAGGGA 556
Db 922 AGCCACTGGAAAGGCA 937
Search completed: March 9, 2006, 23:11:32
Job time : 475.5 secs

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 23:11:40 ; Search time 141.5 Seconds
(without alignments)
6984.624 Million cell updates/sec

Title: US-10-686-428A-3_COPY_444_999

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
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8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	455.2	81.9	2876	3	US-08-840-204-1
3	455.2	81.9	2876	3	US-09-324-494A-1
4	455.2	81.9	2876	3	US-09-324-494A-10
5	455.2	81.9	2876	3	US-09-023-655-1187
6	98.6	17.7	1191	3	US-09-016-434-1210
7	98.6	17.7	2029	9	5495001-6
8	97	17.4	2029	9	5187089-1
9	97	17.4	2029	9	5457090-1
10	97	17.4	2031	9	5495001-8
11	97	17.4	2032	9	5187089-3
12	97	17.4	2032	9	5457090-3
13	74.8	13.5	1564	3	US-08-948-997-1
14	74.8	13.5	1564	3	US-09-348-817A-1
15	74.8	13.5	1564	3	US-09-722-292-1
16	74.8	13.5	1781	3	US-09-566-921-82
17	74.4	13.4	1275	3	US-10-113-113-3
18	73.8	13.3	1539	3	US-09-016-434-44
19	73.8	13.3	1538	2	US-08-487-823B-1
20	73.8	13.3	1558	2	US-08-997-040-1
21	73.8	13.3	1558	2	US-09-203-237-1
22	73.6	13.2	1185	3	US-09-023-339-3
23	73.6	13.2	1260	3	US-09-023-173-5
24	73.6	13.2	1308	3	US-09-023-173-10

25	73.6	13.2	1308	3	US-09-023-339-6
26	72.6	13.1	1152	2	US-08-315-831A-13
27	72.6	13.1	1152	2	US-08-662-318-13
28	72.6	13.1	1152	6	PCT-US95-12509-13
29	72.6	13.1	1316	2	US-07-755-461A-12
30	72.6	13.1	1316	2	US-08-315-831A-12
31	72.6	13.1	1316	2	US-08-662-318-12
32	72.6	13.1	1316	6	PCT-US95-12509-12
33	72.6	13.1	1430	3	US-09-016-434-710
34	71.8	12.9	429	3	US-09-270-767-190
35	71.8	12.9	429	3	US-09-270-767-15472
36	71	12.8	1427	2	US-07-994-133-1
37	71	12.8	1427	9	5196304-1
38	69.4	12.5	1370	3	US-09-026-408-12
39	69.4	12.5	1370	3	US-09-902-684-12
40	69.4	12.5	1370	3	US-10-628-395-12
41	69.4	12.5	1371	3	US-09-026-408-1
42	69.4	12.5	1371	3	US-09-902-684-1
43	69.4	12.5	1371	3	US-10-628-395-1
44	69.4	12.5	1432	3	US-09-023-655-547
45	69.4	12.5	1434	3	US-09-016-434-456

ALIGNMENTS

RESULT 1
US-08-840-204-1
; Sequence 1, Application US/08840204
; Patent No. 6103498
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, DANIEL A.
; APPLICANT: STEFANSSON, STEINGRIMUR P.
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
; TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,204
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: 30807-20004:00
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 76..1281
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 145

[illegible]

/	FILING DATE:		
/	CLASSIFICATION: 435		
/	ATTORNEY/AGENT INFORMATION:		
/	NAME: LIVNAT, SHMUEL		
/	REGISTRATION NUMBER: 33,949		
/	REFERENCE/DOCKET NUMBER: 30807-20004.00		
/	TELECOMMUNICATION INFORMATION:		
/	TELEPHONE: (202) 887-1500		
/	TELEFAX: (202) 822-0168		
/	TELEX: 90-4030 MRSNFORSWSH		
/	INFORMATION FOR SEQ ID NO: 10:		
/	SEQUENCE CHARACTERISTICS:		
/	LENGTH: 2876 base pairs		
/	TYPE: nucleic acid		
/	STRANDEDNESS: double		
/	TOPOLOGY: linear		
/	ANTI-SENSE: YES		
/	US-08-840-204-10		
Query Match 81.9%; Score 455.2; DB 3; Length 2876;			
Best Local Similarity 88.7%; Pred. No. 2.5e-118;			
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;			
QY	1	AAGGAGCTCATGGGGCCGTGGGAACAAAGAATGAGATCAGCACCGGCCGATCCCATCTTTCGTG	60
DB	2495	AAGGAGCTCATGGGCCTTGTAACCAAGAGTAGATCAGCACCGACCACACAGCGATCTTCGTG	2436
QY	61	CAGCGGAGCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTTCAGGCTGTTCCGGACC	120
DB	2435	CAGCGGAGCTGAAGCTGGTCCAGGGCTTCATGCCCTCTCTTTCAGGCTGTTCCGGAGC	2376
QY	121	ACGGTCAAGCAGTGATTTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG	180
DB	2375	ACGGTCAAGCAAGTGACATTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG	2316
QY	181	GTCAGAGACACACAAGGCGATGATCAATGACTTACTTGGCCAAGGGCTGTGGACCCAG	240
DB	2315	GTGAAGACACACAAGAGATATGATCAGCACTTCGTTGGGAAGAGAGCCGTGGACCCAG	2256
QY	241	CTGACGCGCTGGTTCCTGGTGAATGCCCTCTAATCAACGGCCAGTGGAAAAACGCCCTTC	300
DB	2255	CTGACACGGCTGGTGTGGTGAATGCCCTCTAATCAACGGCCAGTGGAAAGACTCCCTTC	2196
QY	301	CCAGAAAAGCACTCACACACGCTCTTCCCAAAGTCATGGGAGACACCGTCTCTGTG	360
DB	2195	CCCAGCTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCAGCTGTCTGTG	2136
QY	361	CCCATCATGGCTCAGAACCAACAGTTCAACTACCTAGTGTTCACCCCCCGACGCCAT	420
DB	2135	CCCATATGGCTCAGAACCAACAGTTCAACTACTGTAGTTTCAACGCCGCGATGCCAT	2076
QY	421	TACTACGACATCTGGAAATTGCCCTACACGGCAACACTCTCAGCATGTTTCATTGCGCC	480
DB	2075	TACTACGATCTCTGGAACTGCGCTACACGGGGACACCTCAGCATGTTTCATTGCGCC	2016
QY	481	CCCTACGAAAAAGAGTGCTCTCTCCGCCCTCACACGATTTCTGGACGCTCAGCTCATC	540
DB	2015	CCATTATAAAAAAGAGTGCTCTCTCTGCCCCCTACCAACATTCGTAGTGCCAGCTCATC	1956
QY	541	AGCCAGTGGAAAGGA 556 	
DB	1955	AGCCACTGGAAAGGCA 1940 	

RESULT 3
US-09-324-494A-1
; Sequence 1, Application US/09324494A
; Patent NO. 6489143
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, Daniel A
; APPLICANT: STEFANSSON, Steingrímur P
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THEREOF
; FILE REFERENCE: 30523/167

; CURRENT APPLICATION NUMBER: US/09/324,494A
; CURRENT FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1281)
; OTHER INFORMATION:
US-09-324-494A-1

Query Match 81.9%; Score 455.2; DB 3; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2.5e-118;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGACGCGCGGATGCCATCTTCGTG 60
DB 382 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGACGCGCGGATGCCATCTTCGTG 441
QY 61 CAGCGGATCTGAAGCTGCTCAGGGTTTCATGCCCTTACTTTCAGGCTGTTCGCGACC 120
DB 442 CAGCGGATCTGAAGCTGCTCAGGGTTTCATGCCCTTACTTTCAGGCTGTTCGCGACC 501
QY 121 ACGGTCAAGCAGTGGATTTTTCAGAGATGAGACGACGAGGTTTCATCAATGACTGG 180
DB 502 ACGGTCAAGCAGTGGATTTTTCAGAGATGAGACGACGAGGTTTCATCAATGACTGG 561
QY 181 GTCAAGAGACACACAAAGGATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCG 240
DB 562 GTCAAGAGACACACAAAGGATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCG 621
QY 241 CTGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 622 CTGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681
QY 301 CCAGAGAAAGACTCAGACACCGCTTCTCCAAAGTCTGATGGGACGACCGCTCTGTG 360
DB 682 CCGGACTCCAGCACCCACCGCGCTTCTCCAAATCAGACGCGGACGCTGCTGTG 741
QY 361 CCATGATGCTCAGACCAAGTTCACTACACTGAGTTTTCACCCCGGAGGCGCAT 420
DB 742 CCATGATGCTCAGACCAAGTTCACTACACTGAGTTTTCACCCCGGAGGCGCAT 801
QY 421 TACTAGCATCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTGCGGC 480
DB 802 TACTAGCATCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTGCGGC 861
QY 481 CCTACGAAAGAGTGCTCTCTCCGCCCTCAGCAGATTCGACGCTCAGCTCATC 540
DB 862 CCTATGAAAGAGTGCTCTCTCTGCCCTCAGCAGATTCGACGCTCAGCTCATC 921
QY 541 AGCCAGTGAAGGGA 556
DB 922 AGCCAGTGAAGGGA 937

RESULT 4

US-09-324-494A-10/c
; Sequence 10, Application US/09324494A
; Patent No. 6489143
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, Daniel A
; APPLICANT: STEFANSON, Steingrur P
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES TH
; FILE REFERENCE: 30523/167
; CURRENT APPLICATION NUMBER: US/09/324,494A
; CURRENT FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10

; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-324-494A-10

Query Match 81.9%; Score 455.2; DB 3; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2.5e-118;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGACGCGCGGATGCCATCTTCGTG 60
DB 2495 AAGGAGCTCATGGGCGCTGGAACAAAGATGAGATCAGACGCGCGGATGCCATCTTCGTG 2436
QY 61 CAGCGGATCTGAAGCTGCTCAGGGTTTCATGCCCTTACTTTCAGGCTGTTCGCGACC 120
DB 2435 CAGCGGATCTGAAGCTGCTCAGGGTTTCATGCCCTTACTTTCAGGCTGTTCGCGACC 2376
QY 121 ACGGTCAAGCAGTGGATTTTTCAGAGATGAGACGACGAGGTTTCATCAATGACTGG 180
DB 2375 ACGGTCAAGCAGTGGATTTTTCAGAGATGAGACGACGAGGTTTCATCAATGACTGG 2316
QY 181 GTCAAGAGACACACAAAGGATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCG 240
DB 2315 GTCAAGAGACACACAAAGGATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCG 2256
QY 241 CTGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 2255 CTGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2196
QY 301 CCAGAGAAAGACTCAGACACCGCTTCTCCAAAGTCTGATGGGACGACCGCTCTGTG 360
DB 2195 CCGGACTCCAGCACCCACCGCGCTTCTCCAAATCAGACGCGGACGCTGCTGTG 2136
QY 361 CCATGATGCTCAGACCAAGTTCACTACACTGAGTTTTCACCCCGGAGGCGCAT 420
DB 2135 CCATGATGCTCAGACCAAGTTCACTACACTGAGTTTTCACCCCGGAGGCGCAT 2076
QY 421 TACTAGCATCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTGCGGC 480
DB 2075 TACTAGCATCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTGCGGC 2016
QY 481 CCTACGAAAGAGTGCTCTCTCCGCCCTCAGCAGATTCGACGCTCAGCTCATC 540
DB 2015 CCTATGAAAGAGTGCTCTCTCTGCCCTCAGCAGATTCGACGCTCAGCTCATC 1956
QY 541 AGCCAGTGAAGGGA 556
DB 1955 AGCCAGTGAAGGGA 1940

RESULT 5

US-09-023-655-1187
; Sequence 1187, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/023,655
;; FILING DATE: HEREWITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Zeller, Karen J.
;; REGISTRATION NUMBER: 37,071
;; REFERENCE/DOCKET NUMBER: PA-0001 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 1187:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2876 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GENBANK
;; CLONE: g189541
;; US-09-023-655-1187

Query Match 81.9%; Score 455.2; DB 3; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2.5e-118;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGGAACAAAGATGAGATCAGCACGGCCGATGCCATCTTCGTG 60
DB 382 AAGGAGCTCATGGGCGGTGGGAACAAAGATGAGATCAGCACGGCCGATGCCATCTTCGTG 441

QY 61 CAGCGGATCTGAAGCTGTTCAGGGTTTCATGCCCTTCTTCAGGCTGTTCGGACC 120
DB 442 CAGCGGATCTGAAGCTGTTCAGGGTTTCATGCCCTTCTTCAGGCTGTTCGGACC 501

QY 121 ACGGTCAAGCAGTGTGATTTTTCAGAGTGGACAGCAGCTTCATCATCAATCACTGG 180
DB 502 ACGGTCAAGCAGTGTGATTTTTCAGAGTGGACAGCAGCTTCATCATCAATCACTGG 561

QY 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTCTTGGCCAAAGGGCTGTGGACCAG 240
DB 562 GTGAAGAGACACACAAAAGGATGATCAATGACTTCTTGGCCAAAGGGCTGTGGACCAG 621

QY 241 CTGACGGCTGTGTTCTGTGTAATGCCCTTCTTCAACGGCCAGTGGAAAGCCCTTC 300
DB 622 CTGACGGCTGTGTTCTGTGTAATGCCCTTCTTCAACGGCCAGTGGAAAGCCCTTC 681

QY 301 CCAGAGAAAGCACTCACACCGCTCTTCCAAAGTCTGTGAGCAGCAGCTCTCTGTG 360
DB 682 CCAGACTCAGACACCCACCGCGCTCTTCCAAAGTCTGTGAGCAGCAGCTCTCTGTG 741

QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACCCCGCCAGCCCAT 420
DB 742 CCCATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACCCCGCCAGCCCAT 801

QY 421 TACTACGACATCCTGGAATGCGCTTCAACGGCAACACTCTGAGCATGTTCAATTCGCC 480
DB 802 TACTACGACATCCTGGAATGCGCTTCAACGGCAACACTCTGAGCATGTTCAATTCGCC 861

QY 481 CCCTACGAAAGAGGTGCTCTCTCCGCTCAGCAGCATCTTGGACGCTCAGCTCATC 540
DB 862 CTTTATGAAAGAGGTGCTCTCTCTCCGCTCAGCAGCATCTTGGACGCTCAGCTCATC 921

QY 541 AGCCAGTGGAAAGGA 556
DB 922 AGCCAGTGGAAAGGA 937

RESULT 6
US-09-016-434-1210

;; Sequence 1210, Application US/09016434
;; Patent No. 6500938
;; GENERAL INFORMATION:
;; APPLICANT: Janice Au-Young
;; APPLICANT: Jeffrey J. Seilhamer
;; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
;; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
;; NUMBER OF SEQUENCES: 1490
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 PORTER DRIVE
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/016,434
;; FILING DATE: HEREWITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Zeller, Karen J.
;; REGISTRATION NUMBER: 37,071
;; REFERENCE/DOCKET NUMBER: PA-0002 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 1210:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1191 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GENBANK
;; CLONE: g183063
;; US-09-016-434-1210

Query Match 17.7%; Score 98.6; DB 3; Length 1191;
Best Local Similarity 49.9%; Pred. No. 7.2e-18;
Matches 276; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

QY 1 AAGGAGCTCATGGGCGGTGGGAACAAAGATGAGATCAGCACGGCCGATGCCATCTTCGTG 60
DB 289 AAGGCGATCGTCTCCAAAGAATAAAGACATTTGTGACAGTGGCTAACCGCGTGTGT 348

QY 61 CAGCGGATCTGAAGCTGTTCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGACC 120
DB 349 AAGATGCTCTGAATTTGAAGTGCCTTTTGTACAGGAACAAGATGTTTCCAGTGT 408

QY 121 ACGGTCAAGCAGTGTGATTTTTCAGAGATGACAGCAGCAGTTCATCATCAATCACTGG 180
DB 409 GAGGTCCGGAATGTGAACCTTTGAGGATCCAGCCTTCGCTGTGATTCATCAATGCATGG 468

QY 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTCTTGGCCAGGGCTGTGGACCA- 239
DB 469 GTTAAAAACGAAACAGGGATATGATTGACAATCTGTGTCCCCAGATCTTATTGATGGT 528

QY 240 --GCTGACGCGCTGTGTTCTGTGTAATGCCCTTCTTCAACGGCCAGTGGAAACGCCC 297
DB 529 GTGCTCAGCAGCTGTCTCTGTCAACGAGTGTATTTCAAGGGTCTGTGGAAATCAGCG 588

QY 298 TTCCAGAGAAAGCACTCACACCGCTCTTTCACAAAGTCTGTATGGCAGCAGCCGTCTCT 357
DB 589 TTCCAAACCCGAGAACACAAAGAAACGCACTTTTCGTGGCAGCGCCGCGGAAATCTCTATCAA 648

Query Match	17.7%; Score 98.6; DB 9; Length 2029;
Best Local Similarity	49.9%; Pred. No. 8.9e-18;
Matches	276; Conservative 0; Mismatches 274; Indels 3; Gaps 1;
QY	1 AAGGAGTCTATGGGCGTGGAAACAAGATGAGATCAGACGCCGATGCCATCTTCGTG 60
DB	
DB	433 AAGGCCATCGTCTCCAAAGAATAAAGACATTTGTGACGTGGCTAACGCCGTTTGT 492
QY	61 CAGCGGGAICTGAAGCTGTGTCAGGGTTCATGCCCTACTTCTTCAGGCTGTTCCGGACC 120
DB	
DB	493 AAGAATGCCTCTGAATTTGAAGTGCCCTTTTGTACAGGAACAAGATGTGTTCCAGTGT 552
QY	121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 180
DB	
DB	553 GAGTCCGGAATGTGAACCTTTTGAGGATCCAGCCTCTGCCTGTGATTCATCAATGATG 612
QY	181 GTGAAGAGACACAAAAAGGCATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCA- 239
DB	
DB	613 GTTAAAAATGAACACGAGGATATGATTGACAACTGCTGTGCCAGATCTTATTGATGGT 672
QY	240 --GCTACAGCGCCTGGTTCGTGGTAATGCCCTCTACTTCAAACGCCAGTGGAAAAACGCC 297
DB	
DB	673 GTGCTCACCAGACTGGTCTCGTCCGCAACGCAGTGTATTTCAAGGCTGTGTGGAATCACGG 732
QY	298 TTCCACAGAAAAAGCACTCACACCGCTCTTCCACAAAGTCTCATGCGACACCGCTCTCT 357
DB	
DB	733 TTCCAACCCGAGAACACAAAGAACGCACTTTCGTGCAGCCGACGGGAATCTATCAAA 792
QY	358 GTGCCCATGATGCTCAGACCAACAAGTTCACTACACTGAGTGTTCACACCCCGACGGC 417
DB	
DB	793 GTGCCAATGTGCCCAGGCTCCGTGTTTCGGGTGTGGGTTCGACAAAGTGCCTCCCAATGAT 852

RESULT 9

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5457090-1
; Patent No. 5457090
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,294
; FILING DATE: 03-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO:1:
; LENGTH: 2029
5457090-1

Query Match
Best Local Similarity 17.4%; Score 97; DB 9; Length 2029;
Matches 275; Conservative 0; Mismatches 275; Indels 3; Gaps 1;

QY 1 AAGGAGCTCATGGGCGCGTGGAAAGATGAGATCAGCAGCGCGGATGCCATCTTCGTG 60
Db 432 AAGGCCATCGTCTCCAAAGAAATAAGACATTTGACAGTGGCTAAACGCGTGTGTT 491
QY 61 CAGCGGATCTGAAGTGGTCCAGGTTTCATGCCCTTCTTCCAGGCTGTTCGGACC 120
Db 493 AAGGATGCTCTGAAATGAAGTGCCTTTTGTACAAAGGAAACAAAGATGTGTTCCAGTGT 552
QY 121 ACGGTCAAGCAGGTGATTTTTCAGAGATGAGACAGAGCCAGGTTCATCATCAATCACTGG 180
Db 553 GAGGTCCGAATGTGAATTTTTCAGAGATGAGACAGAGCCAGGTTCATCATCAATCACTGG 612
QY 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTTGGCCAAAGGGCTGTGGAC--- 237
Db 613 GTTAAAAACGAAACAGGAGATGATGACATCTGCTGCCCAAGATCTTATTGATGT 672
QY 238 CAGCTGACCGCGCTGGTTCGTGTAATGCCCTTACTTCAACGGCCAGTGGAAACGCCC 297
Db 673 GTGCTCACCAGACTGGTCTCTCAACGAGTGTATTTCAAGGGTCTGTGGAATCAAG 732
QY 298 TTCCAGAGAAAGCACTCACCACCGCTTCCCAAGTCTGTGAGTGGAGCAGCCGCTCT 357
Db 733 TTCCAAACCGGAGAACAAAGAAACGCACTTTCTGGGAGCGGCGGAAATCCTATCAA 792
QY 358 GTGCCCATGATGGCTCAGACCAACAAAGTTCAACTACACTAGTGTTCACACCCCGACGGC 417
Db 793 GTGCCAATGCTGGCCAGCTCTCCGTGTTCCGGTGGGTGCAAGTGCCTCCCAATGAT 852
QY 418 CATTACTAGCATCCTGGAATGCCCTTACCAACGGCAACACTCTGAGCATGTTCAATGCC 477
Db 853 TTATGTTACAACTTCAATGAACTGCGCTTACCAACGGGAAAGCATCAGCATGCTGATTGCA 912
QY 478 GCCCCTACGAAAGAGAGTGGCTCTTCCGCGCTTACCAAGCATTTCTGGACGCTCAGTCT 537
Db 913 CTGCGACTGAGAGTCCACTCCGCTGTCTGCCATCATCCCAACATCAGCACCAGACC 972
QY 538 ATCAGCCAGTGA 550
Db 973 ATAGACAGTGA 985

RESULT 10
5495001-8
; Patent No. 5495001
; APPLICANT: MCGROGAN, MICHAEL P.; SCOTT, RANDY W.; BAKER,
; JOFFRE B.; SIMONSEN, CHRISTIAN C.
; TITLE OF INVENTION: RECOMBINANT PURIFIED PROTEASE NEXIN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,596
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 111,111
; FILING DATE: 24-AUG-1993
;
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5495001-8
; APPLICATION NUMBER: 25,450
; FILING DATE: 13-MAR-1987
; APPLICATION NUMBER: 871,501
; FILING DATE: 06-JUN-1986
; APPLICATION NUMBER: 870,232
; FILING DATE: 03-JUN-1986
; SEQ ID NO:8:
; LENGTH: 2031
5495001-8

Query Match
Best Local Similarity 17.4%; Score 97; DB 9; Length 2031;
Matches 275; Conservative 0; Mismatches 275; Indels 3; Gaps 1;

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Db 432 AAGGCCATCGTCTCCAAAGAAATAAGACATTTGACAGTGGCTAAACGCGTGTGTT 491
QY 61 CAGCGGATCTGAAGTGGTCCAGGTTTCATGCCCTTCTTCCAGGCTGTTCGGACC 120
Db 492 AAGGATGCTCTGAAATGAAGTGCCTTTTGTACAAAGGAAACAAAGATGTGTTCCAGTGT 551
QY 121 ACGGTCAAGCAGGTGATTTTTCAGAGATGAGACAGAGCCAGGTTCATCATCAATCACTGG 180
Db 552 GAGGTCCGAATGTGAATTTTTCAGAGATGAGACAGAGCCAGGTTCATCATCAATCACTGG 611
QY 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTTGGCCAAAGGGCTGTGGAC--- 237
Db 612 GTTAAAAATGAACAGGAGATGATGACATCTGCTGTCCCAAGATCTTATTGATGT 671
QY 238 CAGCTGACCGCGCTGGTTCGTGTAATGCCCTTACTTCAACGGCCAGTGGAAACGCCC 297
Db 672 GTGCTCACCAGACTGGTCTCTCAACGAGTGTATTTCAAGGGTCTGTGGAATCAAG 731
QY 298 TTCCAGAGAAAGCACTCACCACCGCTTCCCAAGTCTGTGAGTGGAGCAGCCGCTCT 357
Db 732 TTCCAAACCGGAGAACAAAGAAACGCACTTTCTGGGAGCGGCGGAAATCCTATCAA 791
QY 358 GTGCCCATGATGGCTCAGACCAACAAAGTTCAACTACACTAGTGTTCACACCCCGACGGC 417
Db 792 GTGCCAATGCTGGCCAGCTCTCCGTGTTCCGGTGGGTGCAAGTGCCTCCCAATGAT 851
QY 418 CATTACTAGCATCCTGGAATGCCCTTACCAACGGCAACACTCTGAGCATGTTCAATGCC 477
Db 852 TTATGTTACAACTTCAATGAACTGCGCTTACCAACGGGAAAGCATCAGCATGCTGATTGCA 911
QY 478 GCCCCTACGAAAGAGAGTGGCTCTTCCGCGCTTACCAAGCATTTCTGGACGCTCAGTCT 537
Db 912 CTGCGACTGAGAGTCCACTCCGCTGTCTGCCATCATCCCAACATCAGCACCAGACC 971
QY 538 ATCAGCCAGTGA 550
Db 972 ATAGACAGTGA 984

RESULT 11
5187089-3
; Patent No. 5187089
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS WHICH INHIBIT
; ELASTASE
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO:3:
; LENGTH: 2032
5187089-3

Query Match
Best Local Similarity 17.4%; Score 97; DB 9; Length 2032;
Matches 275; Conservative 0; Mismatches 275; Indels 3; Gaps 1;
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QY 121 ACGETCAAGCAGTGGATTTTTCAGAGATGGACAGACCGAGTTCATCATCAATGACTGG 180
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Db 613 GTTAAACAAAGACAGGATATGATGACATCTGCTGCCAGATCTTATTTGATGTT 672
QY 238 CAGCTGAGCGGCTGTTCTGGTGAATGCGCTTACTTCAACGGCCAGTGGAAAAACGCC 297
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RESULT 12

5457090-3
; Patent No. 5457090
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,294
; FILING DATE: 03-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO: 3
; LENGTH: 2032
5457090-3

Query Match 17.4%; Score 97; DB 9; Length 2032;
Best Local Similarity 49.7%; Pred. No. 2.5e-17;
Matches 275; Conservative 0; Mismatches 275; Indels 3; Gaps 1;
QY 1 AAGGAGCTCATGGGCGCTGGAAACAAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
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QY 181 GTGAAGAGACACAAAGGATGATCAATGACTTACTTGGCCAAAGGGGTGGGAC--- 237
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QY 238 CAGCTGAGCGGCTGTTCTGGTGAATGCGCTTACTTCAACGGCCAGTGGAAAAACGCC 297
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Db 793 GTGCCAATGCTGCCAGCTCTCCGTGTTCCGGTGGGTCGACAAAGTGCCTCAATGAT 852
QY 418 CATTACTAGCATCTCTGGAATTCGCTTACCGGCAACACTCTGAGCATGTTTCAATTGCC 477
Db 853 TTATGTACAACTTCAATGAACTGCTCCCTACCGGGAAGCATCAGCATGCTGATTGCA 912
QY 478 GCCCCTACGAAAGAGTGCCTCTCTCGCCCTCACCAGCATTCGAGCGTCAAGTCC 537
Db 913 CTGCCAGTCTGAGAGTCCACTCCGCTGTCTGCCATCATCCACACATCAGCACCAGACC 972
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RESULT 13

US-08-948-997-1
; Sequence 1, Application US/08948997
; Patent No. 608020
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG
; APPLICANT: COLEMAN, TIM
; APPLICANT: LAWRENCE, DANIEL
; TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF
; TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,997
; FILING DATE: Oct-10-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: A. ANDERS BROOKES
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF336
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1564 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 89..1318

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Qy	321	CCGCTCTTCCACAAAGTCTGATGGCAGCACCGTCTCTGTGCCCATGATGGCTCAGACCAA	380
Db	691	CTTTTCTTTTCACTAAAGATGATGAAAGTGAAGTCCAAATTCCAATGATGATCAGCAAGG	750
Qy	381	CAAGTTCAACTACACTGAGTTT	402
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 Job time : 142.5 secs

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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Score	Match	Length			
1	480.8	86.5	2970	6	US-10-368-995-1	Sequence 1, Appli
2	456.4	82.1	2899	8	US-10-741-600-91	Sequence 91, Appl
3	456.4	82.1	3320	8	US-10-741-600-92	Sequence 92, Appl
4	455.2	81.9	1209	6	US-10-128-706-17	Sequence 17, Appl
5	455.2	81.9	1209	9	US-10-512-496-17	Sequence 17, Appl
6	455.2	81.9	1962	6	US-10-368-995-5	Sequence 5, Appli
7	455.2	81.9	2177	9	US-10-852-335A-45	Sequence 45, Appl
8	455.2	81.9	2660	3	US-09-814-353-20146	Sequence 20146, A
9	455.2	81.9	2870	5	US-10-060-036-131	Sequence 131, App
10	455.2	81.9	2876	6	US-10-128-706-5	Sequence 5, Appli
11	455.2	81.9	2876	6	US-10-170-385-236	Sequence 236, App
12	455.2	81.9	2876	6	US-10-259-609-1	Sequence 1, Appli
13	455.2	81.9	2876	6	US-10-259-609-10	Sequence 10, Appl
14	455.2	81.9	2876	6	US-10-368-995-3	Sequence 3, Appli
15	455.2	81.9	2876	7	US-10-197-258-1	Sequence 1, Appli
16	455.2	81.9	2876	7	US-10-231-958A-419	Sequence 419, App
17	455.2	81.9	2876	7	US-10-641-643-1187	Sequence 1187, Ap
18	455.2	81.9	2876	9	US-10-956-157-442	Sequence 442, App
19	455.2	81.9	2876	9	US-10-512-496-5	Sequence 5, Appli
20	455.2	81.9	2876	9	US-10-506-406-1	Sequence 1, Appli
21	455.2	81.9	2876	9	US-10-631-467-399	Sequence 399, App
22	455.2	81.9	2937	8	US-10-775-163-229	Sequence 229, App
23	455.2	81.9	3171	6	US-10-240-965-160	Sequence 160, App

24	455.2	81.9	3172	5	US-10-044-090-842	Sequence 842, App
25	455.2	81.9	3172	5	US-10-084-817-6	Sequence 6, Appli
26	453.6	81.9	1482	5	US-10-193-658-9	Sequence 9, Appli
27	452	81.3	2970	6	US-10-368-995-7	Sequence 7, Appli
28	420	75.5	3053	6	US-10-128-706-15	Sequence 15, Appli
29	420	75.5	3053	6	US-10-368-995-13	Sequence 13, Appli
30	420	75.5	3053	6	US-10-388-934-233	Sequence 233, App
31	420	75.5	3053	7	US-10-191-803-27	Sequence 27, Appli
32	420	75.5	3053	7	US-10-152-119A-1517	Sequence 1517, Ap
33	420	75.5	3053	9	US-10-512-496-15	Sequence 15, Appli
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35	412	74.1	2999	6	US-10-368-995-11	Sequence 11, Appli
36	412	74.1	2999	9	US-10-764-420-2738	Sequence 2738, Ap
37	412	74.1	2999	9	US-10-631-467-1268	Sequence 1268, Ap
38	319	57.4	473	3	US-09-918-995-11631	Sequence 11631, A
39	299	53.8	425	3	US-09-918-995-8727	Sequence 8727, Ap
40	295.8	53.2	543	7	US-10-231-956A-413	Sequence 413, App
41	280	50.4	387	7	US-10-231-956A-412	Sequence 412, App
42	216.2	38.9	301	7	US-10-231-956A-414	Sequence 414, App
43	172.8	31.1	246	3	US-09-864-761-17528	Sequence 17528, A
44	172.8	31.1	17509	3	US-09-880-107-2097	Sequence 2097, Ap
45	172	30.9	24313	8	US-10-741-600-17587	Sequence 17587, A

ALIGNMENTS

RESULT 1
 US-10-368-995-1
 ; Sequence 1, Application US/10368995
 ; Publication No. US20030217371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vaughan, Douglas E.
 ; APPLICANT: Eren, Mesut
 ; APPLICANT: Declerk, Paul J.
 ; TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON-
 ; TITLE OF INVENTION: ANIMAL
 ; FILE REFERENCE: 1242/43
 ; CURRENT APPLICATION NUMBER: US/10/368,995
 ; CURRENT FILING DATE: 2003-02-19
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 2970
 ; TYPE: DNA
 ; ORGANISM: Cow
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (122)..(1330)
 ; OTHER INFORMATION:
 US-10-368-995-1

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Query Match      86.5%; Score 480.8; DB 6; Length 2970;
Best Local Similarity 91.5%; Pred. No. 1.2e-143;
Matches 509; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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488	CAGCGGACCTAGAGCTGGTCCATGTGTTTCATGCCCACTTCTTCAGGCTGTCCGTACC	547
121	ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGGCCAGGTTTCATCATCAATGACTGG	180
548	ACGGTCAAGCAGGTTGACTTCTCTGAAGTGGAGAGAGCCAGGTTTCATCGTCAACGACTGG	607
181	GTGAAGGACACACAAAGCATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCG	240
608	GTGAAAGACACACAAAGGCATGATCAGCGACTTACTTGGTGAAGGGGGCTGTGGACCAG	667
241	CTGACGCGCCTGGTTCTGGTGAATGCCCTCTACTTCAACGCCACAGTGGAAACGCCCTTC	300

Db 668 CTGACAGCGCTGGTCTGGTAAATGCGCTCTACTTCAACGGCCAGTGAAGATGCGCTTC 727
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCACAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 728 CCAGAGTCAAAACACCCACACCGCTCTTCCACAGTCCGATGGCAGCACCATCTCTGTG 787
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Db 788 CCCATGATGGCTCAGACCAACAAAGTTCAAATACACTGAGTTTACCAACCCCGACGGCGT 847
QY 421 TACTACGACATCTGGAATGGCTTACCAACGGCAACACTCTGAGCATGTTCAATGCGCC 480
Db 848 TACTACGACATCTGGAATGGCTTACCAACGGCAACACTCTGAGCATGTTCAATGCGCC 907
QY 481 CCTACGAAAAGAGTGCTCTCTCCGCCCTCACAGCATTTCTGAGCTCAGCTCATC 540
Db 908 CCTATGAGAAGAGTGCGCTCTCTGCCCCCTACACAGCATTTCTGATGCTGAGCTCATC 967
QY 541 AGCCAGTGAAGAGGA 556
Db 968 AGCCAGTGAAGAGGA 983

RESULT 2

US-10-741-600-91
; Sequence 91, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 2899
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-91

Query Match 82.1%; Score 456.4; DB 8; Length 2899;
Best Local Similarity 88.1%; Pred. No. 8.3e-136;
Matches 490; Conservative 5; Mismatches 61; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCTGGAAACAAAGATGAGATCAGCACGGCCGATGCCATCTTCGTG 60
Db 589 AAGGAGCTCAVGGGGCCATGGAAACAAAGAYGAGATCAGCACACAGACGCRATCTTCGTG 648
QY 61 CAGCGGATCTGAAGTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCCGGACC 120
Db 649 CAGCGGATCTGAAGTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCCGGACC 708
QY 121 ACGGTCAGCAGGTGATTTTTCAGAGATGACAGACGAGGTTTCATCAATGACTGG 180
Db 709 ACGGTCAGCAGGTGATTTTTCAGAGATGACAGACGAGGTTTCATCAATGACTGG 768
QY 181 GTGAAGACACACAAAAGGATGATGATCAATGACTTACTTGGCCAGGGCTGTGGACCA 240
Db 769 GTGAAGACACACAAAAGGATGATGATCAATGACTTACTTGGCCAGGGCTGTGGACCA 828
QY 241 CTGACGCGCTGGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Db 829 CTGACGCGCTGGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 888
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCACAGTCTGATGGCAGCACCGTCTCTGTG 360
Db 889 CCGGACTCCAGCACCCACCRCCGCTCTTCCACAAATCAGAYGGCAGCATCTCTCTGTG 948
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAAATACACTGAGTTTCCACCCCGACGGCCAT 420

Db 949 CCCATGATGGCTCAGACCAACAAAGTTCAAATACACTGATGTTCCACACCGCCGATGGCCAT 1008
QY 421 TACTACGACATCTGGAATGGCTTACCAACGGCAACACTCTGAGCATGTTCAATGCGCC 480
Db 1009 TACTACGACATCTGGAATGGCTTACCAACGGGACAMCCTCAGCATGTTCAATGCTGCC 1068
QY 481 CCTACGAAAAGAGTGCTCTCTCCGCCCTCACAGCATTTCTGAGTGGCCAGCTCATC 540
Db 1069 CCTATGAGAAGAGTGCTCTCTGCCCCCTACCAACATTTCTGAGTGGCCAGCTCATC 1128
QY 541 AGCCAGTGAAGAGGA 556
Db 1129 AGCCAGTGAAGAGGA 1144

RESULT 3

US-10-741-600-92
; Sequence 92, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-92

Query Match 82.1%; Score 456.4; DB 8; Length 3320;
Best Local Similarity 88.1%; Pred. No. 8.7e-136;
Matches 490; Conservative 5; Mismatches 61; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCTGGAAACAAAGATGAGATCAGCACGGCCGATGCCATCTTCGTG 60
Db 589 AAGGAGCTCAVGGGGCCATGGAAACAAAGAYGAGATCAGCACACAGACGCRATCTTCGTG 648
QY 61 CAGCGGATCTGAAGTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCCGGACC 120
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Db 1129 AGCCACTGGAAAGGCA 1144

RESULT 4
US-10-128-706-17
; Sequence 17, Application US/10128706
; Publication No. US20030199463A1
; GENERAL INFORMATION:
; APPLICANT: ITESCU, SILVIU
; TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1
; FILE REFERENCE: 0575/66601
; CURRENT APPLICATION NUMBER: US/10/128,706
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-128-706-17

Query Match 81.9%; Score 455.2; DB 6; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.4e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCGGTGGAAACAAAGATGAGATCAGACAGCGCGCATGTCATCTTCGTG 60
Db 307 AAGGAGCTCATGGGGCGGTGGAAACAAAGATGAGATCAGACAGCGCGCATGTCATCTTCGTG 60

QY 61 CAGCGGATCTGAAGCTGTCCAGGGTTTCATGCCCTTACTTTCAGGCTGTTCGGAGC 120
Db 367 CAGCGGATCTGAAGCTGTCCAGGGTTTCATGCCCTTACTTTCAGGCTGTTCGGAGC 120

QY 121 ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 180
Db 427 ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 180

QY 181 GTGAAGAGACACAAAGAGCATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA 240
Db 487 GTGAAGAGACACAAAGAGCATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA 240

QY 241 CTGACGCGCTGTGTGTAATGCCCTTACTTCAAGCCAGTGGAAAGCGCCCTTC 300
Db 547 CTGACGCGCTGTGTGTAATGCCCTTACTTCAAGCCAGTGGAAAGCGCCCTTC 300

QY 301 CCAGAGAAAGCACTCACCACCGCCCTTCCCAAGTCTGTGGCCAGACCGCTCTGTG 360
Db 607 CCAGACTCCAGACCCACCGCCCTTCCCAAGTCTGTGGCCAGACCGCTCTGTG 360

QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACATGAGTTTTCACCCCGGAGCCAT 420
Db 667 CCATGATGGCTCAGACCAACAAAGTTCAACTACATGAGTTTTCACCCCGGAGCCAT 420

QY 421 TACTACGATCCTGGAATGGCCCTTACCACGCAACACTCTGAGCATGTTTCATTCGCGC 480
Db 727 TACTACGATCCTGGAATGGCCCTTACCACGCAACACTCTGAGCATGTTTCATTCGCGC 480

QY 481 CCTACGAAAGAGTGGCTCTCTCGGCCCTTCCAGCATTTCTGGACGCTCAGCTCATC 540
Db 787 CCTATGAAAGAGTGGCTCTCTCGGCCCTTCCAGCATTTCTGGACGCTCAGCTCATC 540

QY 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCACTGGAAAGGCA 862

RESULT 5
US-10-512-496-17
; Sequence 17, Application US/10512496
; Publication No. US20050148527A1

; GENERAL INFORMATION:
; APPLICANT: ITESCU, SILVIU
; TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1
; FILE REFERENCE: 0575/66601-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/512,496
; CURRENT FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-512-496-17

Query Match 81.9%; Score 455.2; DB 9; Length 1209;
Best Local Similarity 88.7%; Pred. No. 1.4e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCGGTGGAAACAAAGATGAGATCAGACAGCGCGCATGTCATCTTCGTG 60
Db 307 AAGGAGCTCATGGGGCGGTGGAAACAAAGATGAGATCAGACAGCGCGCATGTCATCTTCGTG 60

QY 61 CAGCGGATCTGAAGCTGTCCAGGGTTTCATGCCCTTACTTTCAGGCTGTTCGGAGC 120
Db 367 CAGCGGATCTGAAGCTGTCCAGGGTTTCATGCCCTTACTTTCAGGCTGTTCGGAGC 120

QY 121 ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 180
Db 427 ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 180

QY 181 GTGAAGAGACACAAAGAGCATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA 240
Db 487 GTGAAGAGACACAAAGAGCATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA 240

QY 241 CTGACGCGCTGTGTGTAATGCCCTTACTTCAAGCCAGTGGAAAGCGCCCTTC 300
Db 547 CTGACGCGCTGTGTGTAATGCCCTTACTTCAAGCCAGTGGAAAGCGCCCTTC 300

QY 301 CCAGAGAAAGCACTCACCACCGCCCTTCCCAAGTCTGTGGCCAGACCGCTCTGTG 360
Db 607 CCAGACTCCAGACCCACCGCCCTTCCCAAGTCTGTGGCCAGACCGCTCTGTG 360

QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTACATGAGTTTTCACCCCGGAGCCAT 420
Db 667 CCATGATGGCTCAGACCAACAAAGTTCAACTACATGAGTTTTCACCCCGGAGCCAT 420

QY 421 TACTACGATCCTGGAATGGCCCTTACCACGCAACACTCTGAGCATGTTTCATTCGCGC 480
Db 727 TACTACGATCCTGGAATGGCCCTTACCACGCAACACTCTGAGCATGTTTCATTCGCGC 480

QY 481 CCTACGAAAGAGTGGCTCTCTCGGCCCTTCCAGCATTTCTGGACGCTCAGCTCATC 540
Db 787 CCTATGAAAGAGTGGCTCTCTCGGCCCTTCCAGCATTTCTGGACGCTCAGCTCATC 540

QY 541 AGCCAGTGGAAAGGGA 556
Db 847 AGCCACTGGAAAGGCA 862

RESULT 6
US-10-368-995-5
; Sequence 5, Application US/10368995
; Publication No. US20030217371A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Douglas E.
; APPLICANT: Eren, Mesut
; APPLICANT: Declerk, Paul J.
; TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON-
; FILE REFERENCE: 1242/43
; CURRENT APPLICATION NUMBER: US/10/368,995
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: PatentIn version 3.1
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; SOURCE: PATENT
; SEQ ID NO 5
; LENGTH: 1962
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..
; OTHER INFORMATION:
US-10-368-995-5

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Query Match	81.9%;	Score 455.2;	DB 6;	Length 1962;
Best Local Similarity	88.7%;	Pred. No. 1.7e-135;		
Matches 493;	Conservative	0;	Mismatches 63;	Indels 0;
				Gaps 0;

Qy	1	AAGGAGCTCATGGGGCGTGGAA	CAAAGATGAGATCAGCAGGCCGATGCCATCTTCGTG	60
Dδ	259	AAGGAGCTCATGGGGCGTGGAA	CAAGGATGAGATCAGCACCAAGCGGATCTTCGTC	318

Qy 61 CAGCGGATCTGAAGCTGGTCAGGGTTTCATGCCCTACTTCTTCAGCGTGTCCGGACC 120

Dh 319 CAGCGGCATCTCAAGCTGGTCTCAGGGTTTCATGCCCTACTTCTTCAGCGTGTCCGGAGC 178

[illegible]

QY 181 GTGAAGAGACACACAAAGGCATGATCAATGACTTACTTGCCAAGGGGCTGTGGACCAG 240

QY 241 CTGACGGCCTCGTTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAACGCCCTTC 300

301 CCAGAGAAAAGCACTACCA CGCCTCTTCCAAAGTCTGATGGCAGCACCGTCTCTGTG 360

559	CCCGACATCCAGGACATCCACACCGCCGCTCTTCCACGAAATCGACGCGGACGACATGTCCTCTGTA	618	
QY	361	CCCATGATGGCTCAGACCAACAAAGTTTCAACTACACTGAGTTTTCCACCCCGGACGGCCAT	420

DB	619	CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTACTGAGTTTCAACACGCCCCGATGGCCAT	618
QY	421	TACTACGACATCCTGGAAATTGCCCTACACGCGCAACTCTGAGCATCTTCAATTGCCGCC	480

DB	679	TACTACGACATCTCTGGAACTGCCCTACACGGGGACACCCCTCAGCATATGTTCTATGCTGCC	738
QY	481	CCCTACGAAAAAGAGGTGCCTCTCTCGGCCCTCACGAGCATTTCTGGACGCTCAGCTCATC	540

Db	739	CCTTATGAAAAAGAGGTGCCTCTCTCTGCCCCTCACCAACATTCGTAGTGCCCGAGTCATC	798
Qy	541	AGCCACTGGAAAGGGA	556

Db 799 AGCCACTGGAAAGGCA 814

US-10-852-335A-45
; Sequence 45, Application US/10852335A
; Publication No. US20050112129A1

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: FILE REFERENCE: ES10JRI-US
:
: CURRENT APPLICATION NUMBER: US/10/852,335A
:
: CURRENT FILING DATE: 2004-05-24
:
: PRIOR APPLICATION NUMBER: US 60/548,299
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SEQ ID NO 45

; LENGTH: 2177
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-852-335A-4

Query Match	81.9%	Score 455.2;	DB 9;	Length 2177;
Best Local Similarity	88.7%;	Pred. No. 1.8e-135;		
Matches 493;	Conservative	0;	Mismatches 63;	Indels 0;
				Gaps 0;

Qy 1 AAGGAGCTCATGGGGCGGTGGNACAAAGATGAGATCAGCACGGGCCGATGCCATCTTCGTG 60

Dδ 414 AAGGAGCTCATGGGGCGGTGGNACAAAGATGAGATCAGCACGGGCCGATCTTCGTG 473

Accession	Sequence	Length
Qy	61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCCGGACC	120
Db	474 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCCGGAGC	513

	QY	QY	DB
121	ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG	180	
524	ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG	593	

QY 181 GTGAAGAGACACACAAAGGCATGATCAATGACTTTACTTTGGCCAGGGGCTGTGGACGAG 240

Qy 241 CTGACGGCCTGGTTCGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAACGCCCTTC 300

Qy CCAGAGAAAGCACTCACCACGGCCTTCTCCACAAGTCTGATGGCGACACCGTCTCTGTG 360

CCGACATCTCCAGACACCCACACCCCGCCCTTCTCCAGATTTTCCACCCCGACCGCCAT 420

DB	QY	421	774	833
		TACTAGACATCTCTGGAAATTCCTACCGGCAACACTCTGAGCATGTTTCATTGGCGCC	CCCATGATGGCTCAGAGCCAAACAAGTTCACCTATATCTAGTTCACCAACGCCCCGATGGCCAT	

Db	Qy
834	481
TACTACGACATCCTGTGAACACTGCCCTTACCACGGGGACACCCCTCAGCATGTTTCATTGCTGCC	CCCTACGAAAAAGAGGTGCCCTCTCTCCGCCCTCACCCAGCATTTCTGGACGCTCAGCTCATC
893	540
TACTACGACATCCTGTGAACACTGCCCTTACCACGGGGACACCCCTCAGCATGTTTCATTGCTGCC	CCCTACGAAAAAGAGGTGCCCTCTCTCCGCCCTCACCCAGCATTTCTGGACGCTCAGCTCATC

D _b	CCTTATGAAAAAGAGGTGCCTCTCTCTGGACCATTTCTGAGTGCCAGCTC	953
Q _y	894 ACCTGCGTAAGAAGGA	556

Db 954 AGCCACTGGAAGGCA 969

US-09-814-353-20146
; Sequence 20146, Application US/09814353
; Publication No. US20030165831A1

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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, ALIIS, AND METHODS FOR
 IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 THERAPY OF OVARIAN CANCER
 FILE REFERENCE: MRI-006B

```

: CURRENT APPLICATION NUMBER: US/09/814,353
:
: CURRENT FILING DATE: 2001-03-21
:
: PRIOR APPLICATION NUMBER: US 60/191,031
:
: PRIOR FILING DATE: 2000-03-21
:

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; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,124
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 60/211,940
 ; PRIOR FILING DATE: 2000-05-25

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; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661

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;; PRIOR FILING DATE: 2000-07-25
;; PRIOR APPLICATION NUMBER: US 60/257,672
;; PRIOR FILING DATE: 2000-12-21
;; NUMBER OF SEQ ID NOS: 22037
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 20146
;; LENGTH: 2660
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-814-353-20146

Query Match 81.9%; Score 455.2; DB 3; Length 2660;
Best Local Similarity 88.7%; Pred. No. 1.9e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGAGCTCATGGGCGCGTGGAAAGATGAGATCAGCAGCGCGCGATGCAATCTTCGTG 60
Db 452 AAGAGCTCATGGGCGCGTGGAAAGATGAGATCAGCAGCGCGCGATGCAATCTTCGTG 511
QY 61 CAGGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTACTTCTCAGGCTGTTCCGGACC 120
Db 512 CAGGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTACTTCTCAGGCTGTTCCGGACC 571
QY 121 ACAGCTCAAGCAGTGGATTTTTCAGAGATGAGATCAGCAGCGCGCGATGCAATCTTCGTG 180
Db 572 ACAGCTCAAGCAGTGGATTTTTCAGAGATGAGATCAGCAGCGCGCGATGCAATCTTCGTG 631
QY 181 GTGAAGAGACACACAAAGGATGATCAATGATCTTCTGCGCAAGGGGCTGTGGACCAG 240
Db 632 GTGAAGAGACACACAAAGGATGATCAATGATCTTCTGCGCAAGGGGCTGTGGACCAG 691
QY 241 CTGACGGCTGGTCTGGTGAATGCCCTTACTTCAAGCGCGAGTGGAAAGCGCCCTTC 300
Db 692 CTGACGGCTGGTCTGGTGAATGCCCTTACTTCAAGCGCGAGTGGAAAGCGCCCTTC 751
QY 301 CCAGAGAAAGAGCTACACCGCTCTTCCAGAGTCTGATGCGAGCAGCGTCTGTG 360
Db 752 CCAGCTCAGACACCCAGCGCGCTCTTCCAGATCAGAGCGAGCATGCTCTGTG 811
QY 361 CCCATGATGCTCAGACCAACAAGTTCACTACATGAGTTTCCACCCCGCAGCGCCAT 420
Db 812 CCCATGATGCTCAGACCAACAAGTTCACTACATGAGTTTCCACCCCGCAGCGCCAT 871
QY 421 TACTAGACATCTGGAATTCCTTACCGGCAACAACCTCAGAGCATGTTTCATGCGGCC 480
Db 872 TACTAGACATCTGGAATTCCTTACCGGCAACAACCTCAGAGCATGTTTCATGCGGCC 931
QY 481 CCTTACGAAAGAGGTGCTCTCTCGCCCTCACCAGCATTTCTGGAGCTCAGCTCATC 540
Db 932 CCTTATGAAAGAGGTGCTCTCTCGCCCTCACCAGCATTTCTGGAGCTCAGCTCATC 591
QY 541 AGCCAGTGGAAAGGGA 556
Db 992 AGCCACTGGAAAGGCA 1007

RESULT 9

US-10-060-036-131

; Sequence 131, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yuqiu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

; FILE REFERENCE: 210121-566

; CURRENT APPLICATION NUMBER: US/10/060,036

; CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 131
;; LENGTH: 2870
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-036-131

Query Match 81.9%; Score 455.2; DB 5; Length 2870;
Best Local Similarity 88.7%; Pred. No. 2e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGAGCTCATGGGCGCGTGGAAAGATGAGATCAGCAGCGCGCGATGCAATCTTCGTG 60
Db 376 AAGAGCTCATGGGCGCGTGGAAAGATGAGATCAGCAGCGCGCGATGCAATCTTCGTG 435
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTACTTCTCAGGCTGTTCCGGACC 120
Db 436 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTACTTCTCAGGCTGTTCCGGACC 495
QY 121 ACAGCTCAAGCAGTGGATTTTTCAGAGATGAGATCAGCAGCGCGCGATGCAATCTTCGTG 180
Db 496 ACAGCTCAAGCAGTGGATTTTTCAGAGATGAGATCAGCAGCGCGCGATGCAATCTTCGTG 555
QY 181 GTGAAGAGACACACAAAGGATGATCAATGATCTTACTTGGCCCAAGGGCTGTGGACCAG 240
Db 556 GTGAAGAGACACACAAAGGATGATCAATGATCTTCTGCGAAAGAGCGCGTGGACCAG 615
QY 241 CTGACGGCTGGTCTGGTGAATGCCCTTACTTCAAGCGCGAGTGGAAAGCGCCCTTC 300
Db 616 CTGACGGCTGGTCTGGTGAATGCCCTTACTTCAAGCGCGAGTGGAAAGCGCCCTTC 675
QY 301 CCAGAGAAAGAGCTACACCGCTCTTCCAGAGTCTGATGGAGCAGCGTCTGTG 360
Db 676 CCAGCTCAGACACCCAGCGCGCTCTTCCAGATCAGAGCGGAGCATGCTCTGTG 735
QY 361 CCATGATGCTCAGACCAACAAGTTCACTACATGAGTTTCCACCCCGCAGCGCCAT 420
Db 736 CCATGATGCTCAGACCAACAAGTTCACTACATGAGTTTCCACCCCGCAGCGCCAT 795
QY 421 TACTAGACATCTGGAATTCGCCCTTACACCGGCAACAACCTCAGAGCATGTTTCATGCGGCC 480
Db 796 TACTAGACATCTGGAATTCGCCCTTACACCGGCAACAACCTCAGAGCATGTTTCATGCGGCC 855
QY 481 CCTTACGAAAGAGGTGCTCTCTCGCCCTCACCAGCATTTCTGGAGCTCAGCTCATC 540
Db 856 CCTTATGAAAGAGGTGCTCTCTCGCCCTCACCAGCATTTCTGGAGCTCAGCTCATC 915
QY 541 AGCCAGTGGAAAGGGA 556
Db 916 AGCCACTGGAAAGGCA 931

RESULT 10

US-10-128-706-5

; Sequence 5, Application US/10128706

; Publication No. US20030199463A1

; GENERAL INFORMATION:

; APPLICANT: ITESCU, SILVIU

; TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1

; FILE REFERENCE: 0575/66601

; CURRENT APPLICATION NUMBER: US/10/128,706

; CURRENT FILING DATE: 2002-04-23

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 2876

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-10-128-706-5

Query Match 81.9%; Score 455.2; DB 6; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Query Match 81.9%; Score 455.2; DB 6; Length 2876;
Best Local Similarity 88.7%; Pred. No. 2e-135;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

1 AAGGAGCTCATGGGGCCGTGGAAACAAAGATGAGATCAGACCGGCCGATGCCATCTTCGTG 60
|||
382 AAGGAGCTCATGGGGCCATGGAAACAAAGATGAGATCAGACCGGCCGATGCCATCTTCGTG 441
|||
61 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 120
|||
442 CAGCGGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGCTGTTCGGACC 501
|||
121 ACGGTCAAGCAGTGGATTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 180
|||
502 ACGGTCAAGCAGTGGATTTTCAGAGATGGACAGAGCCAGGTTTCATCAATCAATGACTGG 561
|||
181 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCCAG 240
|||
562 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGAGCCGTGGACCCAG 621
|||
241 CTGACCGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGGAAAGCCCTTC 300
|||
622 CTGACCGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGGAAAGACTCCCTTC 681
|||
301 CCAGAGAAAGCACTCACCACCGCCTCTTCCAAAGTCTGATGGCAGCACCGCTCTGTG 360
|||
682 CCGGACTCAGACACCCACCGCCGCTCTTCCAAATCAATCAGCGGAGCACTGTCTGTG 741
|||
361 CCATGATGGCTCAGACCAACAAAGTTCAACTACTGAGTTTTCACCCCGCCGAGCCCAT 420
|||
742 CCATGATGGCTCAGACCAACAAAGTTCAACTACTGAGTTTTCACCCCGCCGAGCCCAT 801
|||
421 TACTAGGACATCTGGAATGGCTTACACGGCAACACTCTGAGCATGTTTCAATTCGGCCG 480
|||
802 TACTAGGACATCTGGAATGGCTTACACGGCAACACTCTGAGCATGTTTCAATTCGGCCG 861
|||
481 CCTACGAAAGAGTGCTCTCTCGCCCTCACCAGCATCTGAGCATGTTTCAATTCGGCCG 540
|||
862 CCTATGAAAGAGTGCTCTCTCGCCCTCACCAGCATCTGAGCATGTTTCAATTCGGCCG 921
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541 AGCCAGTGGAAAGGGA 556
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922 AGCCACTGGAAAGGCA 937
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RESULT 11

US-10-170-385-236

; Sequence 236, Application US/10170385

; Publication No. US20030203372A1

; GENERAL INFORMATION:

; APPLICANT: Ward, Neil Raymond

; APPLICANT: Mundy, Christopher Robert

; APPLICANT: Kan, On

; APPLICANT: Harris, Robert Alan

; APPLICANT: White, Jonathan

; APPLICANT: Binley, Katie Mary

; APPLICANT: Rayner, William Nigel

; APPLICANT: Naylor, Stuart

; APPLICANT: Kingsman, Susan Mary

; APPLICANT: Krige, David

; TITLE OF INVENTION: ANALYSIS METHOD

; FILE REFERENCE: 532682000100

; CURRENT APPLICATION NUMBER: US/10/170,385

; CURRENT FILING DATE: 2002-06-12

; PRIOR FILING DATE: PCT/GB02/01662

; PRIOR FILING DATE: 2002-04-08

; PRIOR FILING DATE: PCT/GB01/05458

; PRIOR FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 549

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 236

; TYPE: DNA

; LENGTH: 2876

; ORGANISM: Homo Sapiens

US-10-170-385-236

Query Match 81.9%; Score 455.2; DB 6; Length 2876;

Best Local Similarity 88.7%; Pred. No. 2e-135;

Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

RESULT 12

US-10-259-609-1

; Sequence 1, Application US/10259609

; Publication No. US20030216321A1

; GENERAL INFORMATION:

; APPLICANT: LAWRENCE, Daniel A

; APPLICANT: STEFANSON, Steingrimsur P

; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THE

; FILE REFERENCE: 30523/167

; CURRENT APPLICATION NUMBER: US/10/259,609

; CURRENT FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: US/09/324,494A

; PRIOR FILING DATE: 1999-06-02

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 2876

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (76)..(1281)

; OTHER INFORMATION:

US-10-259-609-1

[illegible]

RESULT 15

US-10-197-258-1

03-10-197-238-1
; Sequence 1: Application US/10197258

; sequence 1, Application US/1015
: Publication No. US20040014190A1; PUBLICATION NO. US20
: GENERAL INFORMATION:
: GENERAL INFORMATION:

GENERAL INFORMATION: DANTEL, A

APPLICANT: LAWRENCE, DANIEL A.

APPLICANT: GORLATOVA, NATALIA

APPLICANT: CRANDALL, DAVID L.
TITLE OF INVENTION: MUTANT PROTEINASE-INHIBITORS AND USES THEREOF

; TITLE OF INVENTION: MUTANT
: FILE REFERENCE: 030523-0187

FILE REFERENCE: 030523-0187
CURRENT APPLICATION NUMBER: IIS/1A/107 250

; CURRENT APPLICATION NUMBER: US/1
 ; CURRENT FILING DATE: 2003-07-19

; CURRENT FILING DATE: 2002-
 : NUMBER OF SEC TO NOS: 12

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; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: DotPlotter v2.1

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; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 1

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; LENGTH: 2876

; TYPE: DNA

ORGANISM: Homo sapiens

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; FEATURE:

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; NAME/KEY: CDS

; LOCATION: (

Query Match	81.9%	Score 455.2	DB 7	Length 2876
Best Local Similarity	88.7%	Pred. No. 2e-135		
Matches 493	Conservative	0	Mismatches 63	Indels 0
				Gaps 0

Qy	1	AAGGAGCTCATGGGCGGTGAAACAAGATGAGATCAGCAGCGCGATGCCATCTTCGTG	60
Db	382	AAGGAGCTCATGGGCGCATGNAANAAGATGAGATCAGCACACAGACGATCTTCGTC	441
Qy	61	CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCGCGACC	120
Db	442	CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTCTTCAGGCTGTTCGCGACC	501
Qy	121	ACGCTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG	180
Db	502	ACGCTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTTCATCAATGACTGG	561
Qy	181	GTGAAGAGACACACAAAGGCATGATCAATGACTTACTTGGCCAAGGGGCTGTGGACCGAG	240

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 10, 2006, 01:21:06 ; Search time 322 Seconds

(without alignments)
3984.028 Million cell updates/sec

Title: US-10-686-428A-3_COPY_444_999

Perfect score: 556.

Sequence: 1 aaggagctcatggggcgctg.....catcagccatgaaagggga 556

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA New:

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- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	455.2	81.9	1209	US-10-821-234-729	Sequence 729, App
2	455.2	81.9	2522	US-11-094-519A-11	Sequence 11, Appl
3	455.2	81.9	2876	US-11-091-883-114	Sequence 114, App
4	455.2	81.9	2937	US-10-775-169-229	Sequence 229, App
5	455.2	81.9	3273	US-11-091-883-113	Sequence 113, App
6	420	75.5	3053	US-11-136-527-3753	Sequence 3753, App
7	394.2	70.9	2438	US-11-094-519A-10	Sequence 10, Appl
8	176.6	31.8	1404	US-10-750-185-46781	Sequence 46781, A
9	176.6	31.8	1404	US-10-750-623-46781	Sequence 46781, A
10	157.6	28.5	14302	US-11-136-527-3649	Sequence 3649, App
11	98.6	17.7	1191	US-11-245-147-95	Sequence 95, Appl
12	98.6	17.7	1197	US-10-821-234-636	Sequence 636, App
13	98.6	17.7	2129	US-11-186-284-184	Sequence 184, App
14	96.6	17.4	1963	US-11-136-527-1947	Sequence 1947, App
15	93.2	16.8	1212	US-11-245-147-20	Sequence 20, Appl
16	80.8	14.5	1398	US-10-959-322-2	Sequence 2, Appl
17	74.8	13.5	1559	US-10-955-054A-47	Sequence 47, Appl
18	74.6	13.4	1378	US-11-128-061-873	Sequence 873, App
19	74.6	13.4	1378	US-11-128-049-873	Sequence 873, App
20	69.4	12.5	1370	US-11-048-774-12	Sequence 12, Appl

21	69.4	12.5	1371	9	US-11-048-774-1	Sequence 1, Appl
22	69	12.4	1736	8	US-10-995-561-409	Sequence 409, App
23	69	12.4	1911	8	US-10-995-561-410	Sequence 410, App
24	68.2	12.3	2081	12	US-11-128-061-1036	Sequence 1036, App
25	68.2	12.3	2081	12	US-11-128-049-1036	Sequence 1036, App
26	67.8	12.2	1900	8	US-10-775-169-49	Sequence 49, Appl
27	67.8	12.2	1900	12	US-11-091-883-135	Sequence 135, App
28	67.6	12.2	1299	7	US-10-959-322-40	Sequence 40, Appl
29	67.6	12.2	1395	7	US-10-959-309-18	Sequence 18, Appl
30	67.6	12.2	1395	7	US-10-959-322-1	Sequence 1, Appl
31	67.6	12.2	1599	9	US-11-129-861-43	Sequence 43, Appl
32	66.2	11.9	1918	8	US-10-821-234-48	Sequence 48, Appl
33	65.2	11.7	1254	12	US-11-147-047-13	Sequence 13, Appl
34	64.8	11.7	1782	12	US-11-178-134-13	Sequence 13, Appl
35	64.6	11.6	1398	12	US-11-136-527-309	Sequence 309, App
36	64.2	11.5	1400	12	US-11-136-527-6043	Sequence 6043, App
37	63.2	11.4	1466	8	US-10-776-233A-14	Sequence 14, Appl
38	63.2	11.4	2480	9	US-11-072-512-1410	Sequence 1410, App
39	62.8	11.3	1606	8	US-10-995-561-278	Sequence 278, App
40	62.8	11.3	1655	8	US-10-995-561-277	Sequence 277, App
41	62.8	11.3	2480	8	US-10-995-561-276	Sequence 276, App
42	61.2	11.0	2941	8	US-10-995-561-242	Sequence 242, App
43	61.2	11.0	3035	8	US-10-995-561-238	Sequence 238, App
44	61.2	11.0	3079	8	US-10-995-561-239	Sequence 239, App
45	61.2	11.0	3124	8	US-10-995-561-240	Sequence 240, App

ALIGNMENTS

RESULT 1

US-10-821-234-729
 ; Sequence 729, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_seq_genes Version 1.0
 ; SEQ ID NO 729
 ; LENGTH: 1209
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-821-234-729

Query Match 81.9%; Score 455.2; DB 8; Length 1209;
 Best Local Similarity 88.7%; Pred. No. 1.3e-123;
 Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY	1	AAGGAGCTCATGGGCGCGTGGACAAAGATGAGATCAGCAGCGCCGATGCCATCTTCGTC	60
Db	307	AAGGAGCTCATGGGCGCGTGGACAAAGATGAGATCAGCAGCGCCGATGCCATCTTCGTC	366
QY	61	CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGGTGTTCGGGACC	120
Db	367	CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTCTTCAGGGTGTTCGGGACC	426
QY	121	ACGGTCAAGCAGGTGATTTTTCAGAGATGGACAGCAGCGGTTCATCATCAATGACTGG	180
Db	427	ACGGTCAAGCAGGTGATTTTTCAGAGATGGACAGCAGCGGTTCATCATCAATGACTGG	486
QY	181	GTCAAGACACACACAAAGGATGATCAATGCTTACTTGGCCAAAGGGCTGTGGACCCAG	240
Db	487	GTCAAGACACACACAAAGGATGATCAATGCTTACTTGGCCAAAGGGCTGTGGACCCAG	546

QY 241 CTGACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAACGCGCTTC 300
DB 547 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCCAAGTCTGTGATGGCAGCAGCCGCTCTGTG 360
DB 607 CCGGACTCAGACACCCACCGCGCTCTTCCCAAAATCAGCGCGCACTGTCTCTGTG 666
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACCTGAGTTTTCACACCCCGCAGCGCCAT 420
DB 667 CCCATGATGGCTCAGACCAACAAAGTTCAACTACCTGAGTTTTCACACCGCGCGCAGTGGCCAT 726
QY 421 TACTAGCAGATCTGGAATTCGCCCTACACGGCAACACTCTGAGCAGATGTTCAATGCGGCC 480
DB 727 TACTAGCAGATCTGGAATTCGCCCTACACGGGACACCTCAGCATGTTTCAATGCTGCC 786
QY 481 CCTACGAAAAGAGTGGCTCTCTCCGCCCTCACACAGATTTCTGACGCTCAGCTCATC 540
DB 787 CTTATGAAAAGAGTGGCTCTCTCTGCCCTCACCAACATTTCTGAGTCCCGAGCTCATC 846
QY 541 AGCCAGTGGAAAGGGA 556
DB 847 AGCCACTGGAAGGCA 862

RESULT 2

US-11-094-519A-11
; Sequence 11, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-094-519A-11

Query Match 81.9%; Score 455.2; DB 12; Length 2522;
Best Local Similarity 88.7%; Pred. No. 1.6e-123;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGGCGCGATGCCATCTTCGTG 60
DB 454 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGGCGCGATGCCATCTTCGTG 513
QY 61 CAGCGGATCTCAAGTGGTCTCAGGCTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 120
DB 514 CAGCGGATCTCAAGTGGTCTCAGGCTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 573
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCGAGGTTTCATCAATGACTGG 180
DB 574 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCGAGGTTTCATCAATGACTGG 633
QY 181 GTGAAGAGACACAAAAGGATGATCAATGACTTTCAGGCGCAAGGGGCTGTGGACCAAG 240
DB 634 GTGAAGAGACACAAAAGGATGATCAATGACTTTCAGGCGCAAGGGGCTGTGGACCAAG 693
QY 241 CTGACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAACGCGCTTC 300
DB 694 CTGACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 753
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTTCACAAAGTCTGTGATGGCAGCAGCCGCTCTGTG 360

DB 754 CCCGACTCCAGCACCCACCGCGCTCTTCCAAAATCAGACGGCAGCACTGTCTCTGTG 813
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACCTGAGTTTTCACACCCCGCAGCGCCAT 420
DB 814 CCCATGATGGCTCAGACCAACAAAGTTCAACTACCTGAGTTTTCACACCGCGCGCAGTGGCCAT 873
QY 421 TACTAGCAGATCTCTGGAATTCGCCCTACACGGCAACACTCTGAGCAGATGTTCAATGCGGCC 480
DB 874 TACTAGCAGATCTCTGGAATTCGCCCTACACGGGACACCTCAGCATGTTTCAATGCTGCC 933
QY 481 CCTACGAAAAGAGTGGCTCTCTCCGCCCTCACACAGATTTCTGAGCAGCTCAGCTCATC 540
DB 934 CTTATGAAAAGAGTGGCTCTCTCTGCCCTCACCAACATTTCTGAGTCCCGAGCTCATC 993
QY 541 AGCCAGTGGAAAGGGA 556
DB 994 AGCCACTGGAAGGCA 1009

RESULT 3

US-11-091-883-114
; Sequence 114, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN
; TITLE OF INVENTION: VIABILITY
; FILE REFERENCE: 53942US
; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 114
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-091-883-114

Query Match 81.9%; Score 455.2; DB 12; Length 2876;
Best Local Similarity 88.7%; Pred. No. 1.6e-123;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGGCGCGATGCCATCTTCGTG 60
DB 382 AAGGAGCTCATGGGCGGTGGAAACAAAGATGAGATCAGACGGCGCGATGCCATCTTCGTG 441
QY 61 CAGCGGATCTCAAGTGGTCTCAGGCTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 120
DB 442 CAGCGGATCTCAAGTGGTCTCAGGCTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 501
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCGAGGTTTCATCAATGACTGG 180
DB 502 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCGAGGTTTCATCAATGACTGG 561
QY 181 GTGAAGAGACACAAAAGGATGATCAATGACTTTCAGGCGCAAGGGGCTGTGGACCAAG 240
DB 562 GTGAAGAGACACAAAAGGATGATCAATGACTTTCAGGCGCAAGGGGCTGTGGACCAAG 621
QY 241 CTGACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAACGCGCTTC 300
DB 622 CTGACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 681
QY 301 CCAGAGAAAAGCACTCACACCGCTCTTTCACAAAGTCTGTGATGGCAGCAGCCGCTCTGTG 360
DB 682 CCCGACTCCAGCACCCACCGCGCTCTTTCACAAAATCAGACGGCAGCACTGTCTCTGTG 741

QY 361 CCCATGATGGCTCAGACCAAGTTCACATACAGTGGTTTCCACCCCGAGGGCCAT 420
DB 742 CCCATGATGGCTCAGACCAAGTTCACATACAGTGGTTTCCACCCCGAGGGCCAT 801
QY 421 TACTACGACATCTCTGGAATTCCTCTCCACGCGGCAACACTCTGAGCATGTTTCATTGCGGCC 480
DB 802 TACTACGACATCTCTGGAATTCCTCTCCACGCGGCAACACTCTGAGCATGTTTCATTGCGGCC 861
QY 481 CCCTACGAAAAGAGGTGCCTCTCTCCGCTCTACAGCATCTTGGAGCTCAGCTCATC 540
DB 862 CCTTATGAAAAGAGGTGCCTCTCTCTGCTCTACCAACATCTCTGAGTGGCCAGCTCATC 921
QY 541 AGCCAGTGGAAAGGCA 556
DB 922 AGCCACTGGAAGGCA 937

RESULT 4

US-10-775-169-229
; Sequence 229, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 229
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-229

Query Match 81.9%; Score 455.2; DB 8; Length 2937;
Best Local Similarity 88.7%; Pred. No. 1.6e-123;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGGTGGAAAGATGAGATCAGACGCGCGATGCTCTTGGT 60
DB 250 AAGGAGCTCATGGGCGGTGGAAAGATGAGATCAGACGCGCGATGCTCTTGGT 309
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCCAGGCTGTTCCGGACC 120
DB 310 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCCAGGCTGTTCCGGACC 369
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGACCGAGTTCATCATCAATGACTGG 180
DB 370 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGACCGAGTTCATCATCAATGACTGG 429
QY 181 GTGAAGAGACACAAAGGATGATCAATGATTTTGGCCAGGGGCTGGACCAAG 240
DB 430 GTGAAGAGACACAAAGGATGATCAATGATTTTGGCCAGGGGCTGGACCAAG 489
QY 241 CTGACGCGCTGGTCTGGTGAATGCTCTTCAAGCGGCGAGTGGAAAGCGCCCTTC 300
DB 490 CTGACGCGCTGGTCTGGTGAATGCTCTTCAAGCGGCGAGTGGAAAGCGCCCTTC 549
QY 301 CCAGAGAAAAGCACTCACCACCGCTCTTCCAAAGTCTGATGGCAGACCGTCTCTGTG 360
DB 550 CCGGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGCGAGCACTGTCTGTG 609
QY 361 CCCATGATGGCTCAGACCAAGTTCACATACAGTGGTTTCCACCCCGAGGGCCAT 420
DB 610 CCCATGATGGCTCAGACCAAGTTCACATACAGTGGTTTCCACCCCGAGGGCCAT 669
QY 421 TACTACGACATCTCTGGAATTCCTCTACCAAGGCAACACTCTGAGCATGTTTCATTGCGGCC 480

DB 670 TACTACGACATCTCTGGAATTCCTCTACCAAGGCAACCCCTCAGCATGTTTCATTGCTGCC 729
QY 481 CCCTACGAAAAGAGGTGCCTCTCTCCGCTCTACAGCATCTTGGAGCTCAGCTCATC 540
DB 730 CCTTATGAAAAGAGGTGCCTCTCTCTGCTCTACCAACATCTCTGAGTGGCCAGCTCATC 789
QY 541 AGCCAGTGGAAAGGCA 556
DB 790 AGCCACTGGAAGGCA 805

RESULT 5

US-11-091-883-113
; Sequence 113, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
; TITLE OF INVENTION: VIABILITY
; FILE REFERENCE: 53942US
; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 113
; LENGTH: 3273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (23)..(25)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (28)..(28)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (36)..(36)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (38)..(38)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (40)..(40)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1486)..(1486)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1546)..(1546)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1719)..(1719)
; OTHER INFORMATION: a, c, g, or t
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1835)..(1835)
; OTHER INFORMATION: a, c, g, or t

LENGTH: 3053
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-3753

Query Match 75.5%; Score 420; DB 12; Length 3053;
Best Local Similarity 84.7%; Pred. No. 3.5e-113;
Matches 471; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAGATGAGATCAGACGCGCGGATGCCATCTTCGTG 60
DB 425 AAGGAGCTCATGGGCGCGTGGAAACAAGATGAGATCAGACGCGCGGATGCCATCTTCGTG 484
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 120
DB 485 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 544
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 180
DB 545 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 604
QY 181 GTGAAGAGACACAAAAGCAGTATCAATGACTTACTTGGCCAAAGGGCTGTGGACCAG 240
DB 605 GTGGAGAGGACACAAAAGCAGTATCAATGACTTACTTGGCCAAAGGGCTGTGGACCAG 664
QY 241 CTGACGCGCTGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 665 CTGACGCGCTGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 724
QY 301 CCAGAGAAAGCACTCACACCGCTCTTCCCAAGTCTGATGGCAGCAGCGTCTCTGTG 360
DB 725 TTAGAGCCAGACACCAACGCGCTCTTCCCAAGTCTGATGGCAGCAGCGTCTCTGTG 784
QY 361 CCCATGATGCTCAGACCAACAAAGTTCACACTGAGTTTTCACCGCCCGGACGCCAT 420
DB 785 CCCATGATGCTCAGACCAACAAAGTTCACACTGAGTTTTCACCGCCCGGACGCCAT 844
QY 421 TACTAGCATCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTTGCGGC 480
DB 845 GAGTACGATCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTTGCGGC 904
QY 481 CCTTACGAAAGAGGTCTCTCTCGGCTTCCAGGATCTTGGACGCTCAGCTCATC 540
DB 905 CCTTACGAAAGAGGTCTCTCTCGGCTTCCAGGATCTTGGACGCTCAGCTCATC 964
QY 541 AGCCAGTGGAAAGGA 556
DB 965 AGACATGGAAGCA 980

RESULT 7

US-11-094-519A-10
Sequence 10, Application US/11094519A
Publication No. US2005028181A1

GENERAL INFORMATION:
APPLICANT: BERNSTEIN, Jeanne
APPLICANT: LEVINE, Zurit
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0140P
CURRENT APPLICATION NUMBER: US/11/094,519A
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US/09/695,293
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: IL 132558
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10
LENGTH: 2438
TYPE: DNA
ORGANISM: Homo sapiens
US-11-094-519A-10

Query Match 70.9%; Score 394.2; DB 12; Length 2438;
Best Local Similarity 88.9%; Pred. No. 1.2e-105;
Matches 426; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAGATGAGATCAGACGCGCGGATGCCATCTTCGTG 60
DB 454 AAGGAGCTCATGGGCGCGTGGAAACAAGATGAGATCAGACGCGCGGATGCCATCTTCGTG 513
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 120
DB 514 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCGGGACC 573
QY 121 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 180
DB 574 ACGGTCAAGCAGGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCAATGACTGG 633
QY 181 GTGAAGAGACACAAAAGCAGTATCAATGACTTACTTGGCCAAAGGGCTGTGGACCAG 240
DB 634 GTGAAGAGACACAAAAGCAGTATCAATGACTTACTTGGCCAAAGGGCTGTGGACCAG 693
QY 241 CTGACGCGCTGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 694 CTGACGCGCTGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 753
QY 301 CCAGAGAAAGCACTCACACCGCTCTTCCCAAGTCTGATGGCAGCAGCGTCTCTGTG 360
DB 754 CCGGACTCCAGCACCACCGCGCTCTTCCCAATCAGACGCGCAGCTGTCTCTGTG 813
QY 361 CCCATGATGCTCAGACCAACAAAGTTCACACTGAGTTTTCACCGCCCGGACGCCAT 420
DB 814 CCCATGATGCTCAGACCAACAAAGTTCACACTGAGTTTTCACCGCCCGGACGCCAT 873
QY 421 TACTAGCATCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTTGCGGC 479
DB 874 TACTAGCATCTGGAATGCGCTTACCGGCAACACTCTGAGCATGTTTCATTTGCGGC 932

RESULT 8

US-10-750-185-46781
Sequence 46781, Application US/10750185
Publication No. US20050260603A1

GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 46781
LENGTH: 1404
TYPE: DNA
ORGANISM: Bovine 19866880662738
US-10-750-185-46781

Query Match 31.8%; Score 176.6; DB 8; Length 1404;
Best Local Similarity 90.8%; Pred. No. 8e-42;
Matches 188; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 194 CAAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACGAGCTGACGCGCTGG 253
DB 958 CCATAGGATGATCAGGACTTACTTGGTGAAGGGCTGTGGACGAGCTGACGCGCTGG 1017
QY 254 TTCTGTAATGCCCTCTTACTTCAACGCGCAGTGGAAACGCCCTTCCAGAGAAAGCA 313

Db 1018 TCCTGGTAAATGCCCTCTACTTCAACGGCCAGTGAAGATGCCCTTCCAGAGTCAAAACA 1077
QY 314 CTCACACCGCCCTCTTCCCAAGTCTGATGGCAGCACCGCTCTCTGTGCCCATGATGGCTC 373
Db 1078 CCCACACCGCCCTCTTCCCAAGTCCGATGGCAGCACCATCTCTGTGCCCATGATGGCTC 1137

QY 374 AGACCAACAAGTTCAACTACACTGAGT 400
Db 1138 AGACCAACAAGTTCAACTACAGTAAGT 1164

RESULT 9
US-10-750-623-46781
; Sequence 46781, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46781
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Bovine 19866880662738
US-10-750-623-46781

Query Match 31.8%; Score 176.6; DB 8; Length 1404;
Best Local Similarity 90.8%; Pred. No. 8e-42; Indels 0; Gaps 0;
Matches 188; Conservative 0; Mismatches 19;
QY 194 CAAAGGCATGATCAATGACTTACTTGGCCAAAGGGGCTGTGACACAGCTGACGCGCTGG 253
Db 958 CCATAGGCATGATCAGCGACTTACTTGGTGAAGGGCTGTGACACAGCTGACACGCTGG 1017
QY 254 TCTCGTGAATCCCTCTACTTCAACGGCCAGTGAAGACGCCCTTCCAGAGAAAGCA 313
Db 1018 TCCTGGTAAATGCCCTCTACTTCAACGGCCAGTGAAGATGCCCTTCCAGAGTCAAAACA 1077
QY 314 CTCACACCGCCCTCTTCCCAAGTCTGATGGCAGCACCGCTCTCTGTGCCCATGATGGCTC 373
Db 1078 CCCACACCGCCCTCTTCCCAAGTCCGATGGCAGCACCATCTCTGTGCCCATGATGGCTC 1137
QY 374 AGACCAACAAGTTCAACTACACTGAGT 400
Db 1138 AGACCAACAAGTTCAACTACAGTAAGT 1164

RESULT 10
US-11-136-527-3649
; Sequence 3649, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3649
; LENGTH: 14302
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3649

Query Match 28.3%; Score 157.6; DB 12; Length 14302;
Best Local Similarity 85.8%; Pred. No. 5.7e-36;
Matches 175; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGGCCCTGGGAACAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
Db 5159 AAGGAGCTCATGGGGCTCATGGAACAAGAAATGAGATCAGTACTGCGGACGCCATCTTTGTC 5218
QY 61 CAGCGGATCTGAAGCTGCTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGGACC 120
Db 5219 CAGCGGACCTAGAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAAGCTCTTCCGGACC 5278
QY 121 ACGGTCGAAGCAGGTGGATTTTTTCAGAGATGACAGAGCCAGGTTTCATCATCAATGACTGG 180
Db 5279 ACGGTGAAGCAGGTGGACTTCTCAGAGGTGGAAGAGCCAGATTTCATCAACGACTGG 5338
QY 181 GTGAAGACACACAAAGGCATG 204
Db 5339 GTGGAGAGGCACACCAAGGTAGG 5362

RESULT 11
US-11-245-147-95
; Sequence 95, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTROGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; CURRENT FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 95
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-245-147-95

Query Match 17.7%; Score 98.6; DB 9; Length 1191;
Best Local Similarity 49.9%; Pred. No. 6e-19;
Matches 276; Conservative 0; Mismatches 274; Indels 3; Gaps 1;
QY 1 AAGGAGCTCATGGGGCCCTGGGAACAAGATGAGATCAGACGGCCGATGCCATCTTCGTG 60
Db 289 AAGGCGATCGTCTCCAAGAAGATAAAGACATTGTGACAGTGGCTTAACGCCGTGTTGTT 348
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGGACC 120
Db 349 AAGATGCTCTGAAATTGAAGTGCCTTTTGTACAGGAACAAGATGTGTTCAGTGT 408
QY 121 ACGGTCAAGCAGGTGGATTTTTTCAGAGATGACAGAGCCAGGTTTCATCATCAATGACTGG 180
Db 409 GAGTCCGGGAATGTGAACCTTTGAGGATCCAGCCCTCTGCTGTGTGATTCATCAATGACTGG 468

[illegible]

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RESULT 13
US-11-186-284-184
; Sequence 184, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0

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; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 2129
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (210)...(1406)
US-11-186-284-184

Query Match      17.7%; Score 98.6; DB 12; Length 2129;
Best Local Similarity 49.9%; Pred. No. 7.1e-19;
Matches 276; Conservative 0; Mismatches 274; Indels 3; Gaps 17

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Db      498 AAGGCCATCGTCTCCAAGAAGATAAAGACATTGTGCAGTGCGCTACGCCGTGTGTT 557
          ||| |||| |

QY      61 CAGCGGGATCTGAAGCTGTGTCAGGGTTTTCA GCCCTACTTCTTCAGGCTGTTC CGGACC 120
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Qy 259 GTGAATGCCCTCTACTTCAACGGCCAGTGGAACGCCCTTCCAGAGAAAAGCACTCAC 318
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Qy 319 CACCGCCTCTTCCACAAGTCTGATGGCAGACCGTCTCTGTGCCCCATGATGGCTCAGACC 378
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 379 AACAAAGTTCAACTACACTGAGTTTCCACCCCGACGGCCATTACTACGACATCCTGGAA 438
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Qy 681 TCTGTGTCCGCTCAGGGTCTACAGGACCCCGAATGGCTTATGGTACAACTTCATTGAG 740
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Qy 439 TTGCCCTTACCACGGCAACACTCTGAGCATGTTCAATTGCCGCCCTTACGAAAAGAGGTG 498
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Job time : 324 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 23:11:05 ; Search time 5640 Seconds
(without alignments)
4612.344 Million cell updates/sec

Title: US-10-686-428a-3_COPY_444_999
Perfect score: 556
Sequence: 1 agggagctcatgggcccgtg.....catcagccagtgaaaggga 556

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	455.2	81.9	659	CN309034	CN309034 170004247
2	455.2	81.9	813	BG829624	BG829624 602763976
3	455.2	81.9	932	BE905905	BE905905 601495570
4	455.2	81.9	1027	BX396693	BX396693 BX396693
5	455.2	81.9	1168	AY402982	AY402982 Pan trogl
6	455.2	81.9	1209	AY402981	AY402981 Homo sapi
7	455.2	81.9	1474	CR614829	CR614829 full-len
8	454.8	81.8	1019	BX379573	BX379573 BX379573
9	454.8	81.8	1085	BX335507	BX335507 BX335507
10	454.4	81.7	1028	BX425037	BX425037 BX425037
11	453.6	81.6	1116	BX446279	BX446279 BX446279
12	452.6	81.4	817	BI870529	BI870529 603394394
13	450	80.9	894	CA489543	CA489543 AGENCOURT
14	450	80.9	1029	BX382561	BX382561 BX382561
15	444.4	79.9	971	BX417006	BX417006 BX417006
16	444.4	79.9	1017	BX439383	BX439383 BX439383
17	444.4	79.9	1093	BX356157	BX356157 BX356157
18	444.2	79.9	749	BI224426	BI224426 602940982
19	444.2	79.9	829	CD609138	CD609138 56081741J
20	444.2	79.9	1010	BX340248	BX340248 BX340248
21	444.2	79.9	1124	BX378424	BX378424 BX378424
22	443.8	79.8	832	BX379609	BX379609 BX379609

c

Query Match 81.9%; Score 455.2; DB 7; Length 659;
Best Local Similarity 88.7%; Pred. No. 4.3e-115;
Matches 493; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

ALIGNMENTS

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28	441	79.3	931	5	BU540881	BU540881
29	439.8	79.1	853	5	BX344504	BX344504
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33	433.8	78.0	960	5	BX335314	BX335314
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35	432.8	77.8	968	5	BX355763	BX355763
36	432.4	77.8	681	6	CF132569	CF132569
37	427.4	76.9	948	5	BX381412	BX381412
38	424.4	76.3	999	6	CD609140	CD609140
39	421.4	75.8	588	3	BM127625	BM127625
40	421.4	75.8	818	2	BE908739	BE908739
41	419.4	75.4	869	3	BO218607	BO218607
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RESULT 1
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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

FEATURES

source

659 bp mRNA linear EST 16-MAY-2004
17000424711627 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
CN309034.1 GI:47325448
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Bradenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Bradenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbradenberger@geron.com
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Location/Qualifiers
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/note="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

659 bp mRNA linear EST 16-MAY-2004

17000424711627 GRN_EB Homo sapiens cDNA 5', mRNA sequence.

CN309034.1 GI:47325448

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

Bradenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,

Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,

Lebkowski, J. and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that

control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

15146197

Contact: Bradenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbradenberger@geron.com

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Location/Qualifiers

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/db_xref="taxon:9606"

/tissue type="embryonic stem cells, embryoid bodies

derived from H1, H7 and H9 cells"

/clone.lib="GRN_EB"

/note="oligo dt primed, full-length enriched cDNA library

from embryoid body outgrowths derived from hES cell lines

H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free

conditions."

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QY 478 TACTACGACATCCTGGAAATGGCTTACCAACGCGGACACCTCAGCATGTTCAATTCGCC 537
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QY 541 AGCCAGTGGAAAGGCA 556
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LOCUS 602763976F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4899139 5',
DEFINITION mRNA sequence.
ACCESSION BG829624
VERSION BG829624.1 GI:14177211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 813)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1790 row: h column: 20
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Location/Qualifiers
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FEATURES
source

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Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
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for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
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Note: this is a NIH_MGC Library."
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ORIGIN

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DEFINITION mRNA sequence.  
ACCESSION BE905905  
VERSION BE905905.1 GI:10399246  
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QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCCTCGGACC 120
 DB 367 CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTTCTTTCAGGCTGTTCCTCGGACC 426

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RESULT 7

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 full-length cDNA clone CS0D1031YB21 of Placenta Cot 25-normalized
 of Homo sapiens (human).

ACCESSION CR614829

VERSION CR614829.1 GI:50495636

KEYWORDS HTC; CNSLT_CDNA.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 1474)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue

Genoscope.

2 (bases 1 to 1474)

REFERENCE

AUTHORS Direct Submission

TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT

- Web : www.genoscope.cns.fr)
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

FEATURES

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ORIGIN

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 DB 614 GTGAAGAGACACACAAAGGATGATCAATGACTTCTTTCAGGCGGAGGCGGTGGACCCAG 673

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QY 361 CCCATGATGCTCAGACACACAGTTCACACTACAGTGTTCACCGCGGAGGCGCAT 420
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QY 541 AGCCAGTGGAAAGGGA 556
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RESULT 8

BX379573

LOCUS

DEFINITION

ACCESSION BX379573

VERSION BX379573

KEYWORDS EST..

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

BX379573 1019 bp mRNA linear EST 28-APR-2004

BX379573 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CS0D1031YB21 5-PRIME, mRNA sequence.

BX379573.2 GI:46832548

EST..

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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REFERENCE
AUTHORS 1 (bases 1 to 1019)
TITLE    Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
JOURNAL  Full-length cDNA libraries and normalization
COMMENT  Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30459782.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4412.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1035CF07QPI&c=4412.f.
FEATURES
source
Location/Qualifiers
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 81.8%; Score 454.8; DB 5; Length 1019;
Best Local Similarity 88.5%; Pred. No. 6.2e-115;
Matches 492; Conservative 1; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAAGATGAGATCAGCAGCGCGCGATGCCATCTTCGTG 60
DB 432 AAGGAGCTCATGGGCGCGTGGAAACAAAGATGAGATCAGCAGCGCGCGATGCCATCTTCGTG 491
QY 61 CAGCGGATCTGAAGTGGTCAGGGTTTCATGCCCTACTTTCAGGCTGTTCGGACC 120
DB 492 CAGCGGATCTGAAGTGGTCAGGGTTTCATGCCCTACTTTCAGGCTGTTCGGAGC 551
QY 121 ACGGTCACAGCAGTGGATTTTTCAGAGATGGACAGCAGGTTTCATCATCAATCACTGG 180
DB 552 ACGGTCACAGCAGTGGATTTTTCAGAGTGGAGAGCCAGATTCATCATCAATCACTGG 611
QY 181 GTGAAGAGACACACAAAAGGCATGATCAATGACTTACTTTGGCCAAAGGGCTGTGGACCAG 240
DB 612 GTGAAGAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGGTGGACCAG 671
QY 241 CTGACGGCTGTGTTCTGTGTAATGCCCTCTACTTCAACGGCCAGTCAGAAACGCCCTTC 300
DB 672 CTGACACGGCTGTGTTCTGTGTAATGCCCTCTACTTCAACGGCCAGTCAGAAACGCCCTTC 731
QY 301 CCAGAGAAAGACACTCACACCGCTCTTCCACAGTCTGATGGCAGCAGCTCTCTGTG 360
DB 732 CCGGACTCCAGCACCACCGCGCTCTTCCACAAATCAGCGGACAGCTCTCTGTG 791
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTACATGAGTTTTCACCCCGACGCCCAT 420
DB 792 CCCATGATGGCTCAGACCAACAAAGTTCAACTACATGAGTTTTCACCGCCGATGCCCAT 851
QY 421 TACTACGACATCCTGGAAATGGCTTACACCGCAACACTCTGAGCATGTTCAATGCCGCC 480
DB 852 TACTACGACATCCTGGAAATGGCTTACACCGGGACACCCCTCAGCATGTTCAATGCCGCC 911
QY 481 CCTACGAAAGAGGTGCCTCTCTCCGCCCTCACCAGCATCTCGAGCGCTCAGCTCATC 540
DB 912 CTTATGAAAGAGGTGCCTCTCTCTGCCCTCACCAACATTTCTGAGTGCCCGCTCATC 971
QY 541 AGCCAGTGGAAAGGGA 556
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Db 972 AGCCACTGGRAAGCA 987
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RESULT 9
BX335507 1085 bp mRNA linear EST 07-APR-2004
LOCUS BX335507 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1015YB08 5-PRIME, mRNA sequence.
ACCESSION BX335507
VERSION BX335507.2 GI:46266450
KEYWORDS EST.
SOURCE BX335507.2
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1085)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 1, 2003 this sequence version replaced gi:30312419.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4412.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1015DA04QPI&c=4412.f.
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1015YB08"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 81.8%; Score 454.8; DB 5; Length 1085;
Best Local Similarity 88.5%; Pred. No. 6.3e-115;
Matches 492; Conservative 1; Mismatches 63; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCGTGGAAACAAAGATGAGATCAGCAGCGCGCGATGCCATCTTCGTG 60
DB 421 AAGGAGCTCATGGGCGCGTGGAAACAAAGATGAGATCAGCAGCGCGCGATGCCATCTTCGTG 480
QY 61 CAGCGGATCTGAAGTGGTCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGACC 120
DB 481 CAGCGGATCTGAAGTGGTCAGGGTTTCATGCCCTACTTCTTCAGGCTGTTCGGAGC 540
QY 121 ACGGTCACAGCAGTGGATTTTTCAGAGATGGACAGCAGGTTTCATCATCAATCACTGG 180
DB 541 ACGGTCACAGCAGTGGATTTTTCAGAGTGGAGAGCCAGATTCATCATCAATCACTGG 600
QY 181 GTGAAGAGACACACAAAAGGCATGATCAATGACTTACTTTGGCCAAAGGGCTGTGGACCAG 240
DB 601 GTGAAGAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGGTGGACCAG 660
QY 241 CTGACGGCTGTGTTCTGTGTAATGCCCTCTACTTCAACGGCCAGTCAGAAACGCCCTTC 300
DB 661 CTGACACGGCTGTGTTCTGTGTAATGCCCTCTACTTCAACGGCCAGTCAGAAACGCCCTTC 720
QY 301 CCAGAGAAAGACACTCACACCGCTCTTCCCAAGTCTGATGGCAGCAGCGCTCTCTGTG 360
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Db      721  CCCGACTCCAGCACCACCGCGGCTCTTCCACAAATCAGACGGCAGCATGTCCTGTG 780
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Db      781  CCCATGATGCTCAGACCAACAAGTTCACTACACTGAGTTTCCACCGCCGATGGCCAT 840
Qy      421  TACTACGACATCTGGAAATTCCTACCGGCAACACTTGAGCATGTTTCATTCGGCC 480
Db      841  TACTACGACATCTGGAAATTCCTACCGGCAACACTTGAGCATGTTTCATTCGGCC 900
Qy      481  CCCTACGAAAGAGGTGCTCTCTCCGCGCTCACCAGCAATTCGACGCTCAGCTCATC 540
Db      901  CCTTATGAAAGAGGTGCTCTCTCCGCGCTCACCAGCAATTCGAGTCCGAGCTCATC 960
Qy      541  AGCCAGTGGAAAGGGA 556
Db      961  AGCCACTGGAAAGGCA 976

RESULT 10
BX425037
LOCUS   BX425037 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA0082C09
DEFINITION
5-PRIME, mRNA sequence.
ACCESSION BX425037.2 GI:46999418
VERSION    EST.
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1028)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 15, 2003 this sequence version replaced gi:30772430.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4412.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CLOBA0082C09RP1&c=4412.f.

FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBA0082C09"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 81.7%; Score 454.4; DB 5; Length 1028;
Best Local Similarity 88.3%; Pred. No. 8e-115;
Matches 491; Conservative 2; Mismatches 63; Indels 0; Gaps 0;

Qy      1  AAGGAGCTCATGGGCGCGTGGAAACAAAGATGATGATCAGCAGCGCGCATGCCATCTTCGTG 60
Db      438  AAGGAGCTCATGGGCGCGTGGAAACAAAGATGATGATGATCAGCAGCGCGCATCTTCGTC 497

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Qy      61  CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTTCAGGCTGTTCCGGACC 120
Db      498  CAGCGGATCTGAAGCTGGTCCAGGGTTTCATGCCCTACTTCTTTCAGGCTGTTCCGGAGC 557
Qy      121  ACGGTCAAGCAGTGGATTTTTCAGAGATGGACAGAGCCAGGTTTCATCATCAATGACTGG 180
Db      558  ACGGTCAAGCAGTGGATTTTTCAGAGATGGAGAGCCAGGTTTCATCATCAATGACTGG 617
Qy      181  GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCAG 240
Db      618  GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGGCTGTGGACCAG 677
Qy      241  CTGACGGGCTGTTTCTGTTGATGCTTACTTCAACGGCCAGTGGAAAAAGCCCTTC 300
Db      678  CTGACGGGCTGTTTCTGTTGATGCTTACTTCAACGGCCAGTGGAAAAAGCTCCCTTC 737
Qy      301  CCAGAGAAAAGCACTCACCAACGGCTTCTCCAAAGTCTGATGGCAGACCGCTCTCTGTG 360
Db      738  CCGGACTCCAGACCCACCGCGGCTCTTCCAAATCAGACGGCAGCATGTCCTGTG 797
Qy      361  CCGATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTTCACCCCGCAGGCCAT 420
Db      798  CCGATGATGGCTCAGACCAACAAAGTTCAACTACACTGAGTTTCACCAACCGCCGATGGCCAT 857
Qy      421  TACTAGACATCTGGAATTGCCCTACCAAGGCAACACTCTGAGCATGTTTCATTCGGCC 480
Db      858  TACTAGACATCTGGAATTGCCCTACCAAGGCAACACTCTGAGCATGTTTCATTCGGCC 917
Qy      481  CCTACGAAAAGAGGTGCTCTCTCCGCGCTCACCAGCATTTCTGACGCTCAGCTCATC 540
Db      918  CTTATGAAAAGAGGTGCTCTCTCTGCGCTCACCACATTTCTGAGTCCCGCAGCTCATC 977
Qy      541  AGCCAGTGGAAAGGGA 556
Db      978  AGCCACTGGAAAGGCA 993

RESULT 11
BX446279
LOCUS   BX446279 Homo sapiens PLACENTA Homo sapiens cDNA clone
DEFINITION
5-PRIME, mRNA sequence.
ACCESSION BX446279.2 GI:47007413
VERSION    EST.
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1116)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 15, 2003 this sequence version replaced gi:30780405.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4412.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CLOBA0012E03RP1&c=4412.f.

FEATURES
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/organism="Homo sapiens"
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AGENCY: 10810368 MAPcL Homo sapiens cDNA clone IMAGE:6722018 5',
mRNA sequence.
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VERSION C489543.1 GI:24952334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 894)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cyabbs-remail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14284 row: b column: 02
High quality sequence stop: 674.
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/clone="IMAGE:6722018"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
hERT-HMEL, LNCaP"
/lab_host="EMDH10B"
/clone_lib="MAPcL"
/notes="Vector: pCMV-Sport6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkook Lee, & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
ORIGIN
Query Match 80.9%; Score 450; DB 6; Length 894;
Best Local Similarity 88.3%; Pred. No. 1.3e-113;
Matches 489; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGGTGGACAAAGATGATGATCAGACGCGCGATGCCATCTTCGTG 60
DB 298 AAGGAGCTCATGGGCGGTGGACAAAGATGATGATCAGACGCGCGATGCCATCTTCGTG 357
QY 61 CAGCGGGATCTGAAGCTGTGTGTCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCGGACC 120
DB 358 CAGCGGGATCTGAAGCTGTGTGTCAGGGCTTCATGCCCTACTTCTCAGGCTGTTCGGAGC 417
QY 121 ACGGTCAAGCAGGTGATTTTTCAGAGATGGACAGACGAGGTTTCATCATCAATGACTGG 180
DB 418 ACGGTCAAGCAGGTGACTTTTCAGAGGTGGAGAGCCAGATTTCATCATCAATGACTGG 477
QY 181 GTGAGAGACACACAAAGGATGATCAATGATTTACTTGGCCAGGCGCTGTGGACACAG 240
DB 478 GTGAGAGACACACAAAGGATGATCAGCAACTTCTTGGGAAGGAGCGGTGGACACAG 537
QY 241 CTGACGCGCTGTGTGTGTGATGCTCTTCAACGCGCAGTGGAAAGCGCTTC 300
DB 538 CTGACACGCGCTGTGTGTGTGATGCTCTTCAACGCGCAGTGGAAAGCTCCCTTC 597
QY 301 CCAGAGAAAGCACTCACACCGCTCTTCCCAAGTCTGTGGGAGCAGCCGCTCTCTGTG 360
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QY 361 CCCATGATGCTCAGACCAACAGTTCACTACACTGAGTTTCCACCCCGGAGGCCAT 420
DB 658 CCCATGATGCTCAGACCAACAGTTCACTACACTGAGTTTCCACCCCGGAGGCCAT 717
QY 421 TACTACGACATCTCTGGAATTCCTACCGCAACACTCTGAGCATGTTTCATTTGCCGCC 480
DB 718 TACTACGACATCTCTGGAATTCCTACCGCAACACTCTGAGCATGTTTCATTTGCCGCC 777
QY 481 CCTACGAAAGAGGTGCTCTCTCGGCCCTCACCAGCAATTCGACGCTCAGCTCATC 540
DB 778 CTTTATGAAAGAGGTGCTCTCTCGGCCCTCACCAGCAATTCGAGTGCCAGCTCATC 837
QY 541 AGCCAGTGGAAAGG 554
DB 838 AGCCCTTGGAAAG 851
RESULT 14
BX382561
LOCUS BX382561
DEFINITION BX382561 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSOD1082YB17 5-PRIME, mRNA sequence.
ACCESSION BX382561
VERSION BX382561.2 GI:46832678
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1029)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30459067.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4412.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOD1082CA09QP1&c=4412.f.
FEATURES
Location/Qualifiers
1..1029
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1082YB17"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 80.9%; Score 450; DB 5; Length 1029;
Best Local Similarity 87.4%; Pred. No. 1.3e-113;
Matches 486; Conservative 5; Mismatches 65; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGGTGGACAAAGATGATGATCAGACGCGCGATGCCATCTTCGTG 60
DB 437 AAGGAGCTCATGGGCGGTGGACAAAGATGATGATCAGACGCGCGATCTTCGTG 496
QY 61 CAGCGGGATCTGAAGCTGTGTGTCAGGGTTTCATGCCCTACTTCTCAGGCTGTTCGGACC 120
DB 497 CAGCGGGATCTGAAGCTGTGTGTCAGGGCTTCATGCCCTACTTCTCAGGCTGTTCGGAGC 556

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QY 121 ACGGTACAGCAGTGGATTTTTCAGAGATGGACAGGACAGGTCATCATCAATCACTGG 180
Db 557 ACGGTACAGCAGTGGATTTTTCAGAGATGGACAGGACAGGTCATCATCAATCACTGG 616
QY 181 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA 240
Db 617 GTGAAGAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA 676
QY 241 CTGACGCGCTCGTGTGTAATGCGCTTACTTCAACGGCCAGTGGAAAACGCCCTTC 300
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QY 301 CCAGAGAAAAGCACTCACACCGCTCTTCCAAAGTCTGTAGGACGACCGTCTCTGTG 360
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QY 361 CCATGATGGCTCAGACCAAGTTCACACTACACTGATGTTTCCACCCCGACGGCCAT 420
Db 797 CCATGATGGCTCAGACCAAGTTCACACTACACTGATGTTTCCACCCCGACGGCCAT 856
QY 421 TACTACGACATCTCGGAATTGCGCTTACCACGGCAACACTCTCAGCATGTTCAATGCCGCC 480
Db 857 TACTACGACATCTCGGAATTGCGCTTACCACGGGGMACCTCAGMATGTTCAATGCTGCC 916
QY 481 CCTTACGAAAAGAGTGCTCTCTCGCCCTTCCACAGCAATCTGAGCGCTCAGCTCATC 540
Db 917 CCTTATGAAAARAGTGCTCTCTCGCCCTTCCCAAMATTCTGAGTGCCCGAGCTCATC 976
QY 541 AGCCATGGAAGGGA 556
Db 977 AGCCATGGAAGGGA 992
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RESULT 15
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LOCUS BX417006 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE003YG11
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX417006
VERSION BX417006.2 GI:46923165
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 971)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30633206.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4412.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE003AD06QPI&c=4412.f.
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FEATURES

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1..971
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE003YG11"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
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ORIGIN

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Query Match 79.9%; Score 444.4; DB 5; Length 971;
Best Local Similarity 88.7%; Pred. No. 4.7e-112;
Matches 481; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCGGTGGAAACAAGATGAGATCAGACGGCGATGCCATCTTCGTG 60
Db 430 AAGGAGCTCATGGGGCCATGGAAACAAGATGAGATCAGACGACGCGATCTTCGTG 489
QY 61 CAGCGGATCTGAAGCTGCTCAGGGTTTCATGCCCTTACTTCTTCAGGCTGTTCGGAGCC 120
Db 490 CAGCGGATCTGAAGCTGCTCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGCC 549
QY 121 ACGGTCAAGAGGTGATTTTTCAGAGATGGACAGGACGAGGTTCAATCAATCACTGG 180
Db 550 ACGGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTTCATCAATCACTGG 609
QY 181 GTGAAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA 240
Db 610 GTGAAGACACACAAAAGGATGATCAATGACTTACTTGGCCAAAGGGCTGTGGACCA 669
QY 241 CTGACGCGCTCGTGTGTAATGCGCTTACTTCAACGGCCAGTGGAAAACGCCCTTC 300
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Db 970 AG 971
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Search completed: March 10, 2006, 02:39:58
Job time : 5645 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 22:55:45 ; Search time 3287 Seconds
(without alignments)
9615.138 Million cell updates/sec

Title: US-10-686-428A-4_COPY_238_793
Perfect score: 556
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Score	Query Match	Length	ID	Description
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2	556	100.0	1209	11 AY889067	AY889067 Synthetic
3	556	100.0	1209	11 AY891356	AY891356 Synthetic
4	556	100.0	1209	11 AY891655	AY891655 Synthetic
5	556	100.0	1209	11 AY893400	AY893400 Synthetic
6	556	100.0	1209	11 AY893851	AY893851 Synthetic
7	556	100.0	1332	6 CQ716284	CQ716284 Sequence
8	556	100.0	1962	8 HSPA11	X04744 Human mRNA
9	556	100.0	2207	8 BC010860	BC010860 Homo sapi
10	556	100.0	2660	6 CQ413075	CQ413075 Sequence
11	556	100.0	2876	6 AR106060	AR106060 Sequence
12	556	100.0	2876	6 AR106066	AR106066 Sequence
13	556	100.0	2876	6 BD094083	BD094083 Shear str
14	556	100.0	2876	6 CQ776713	CQ776713 Sequence
15	556	100.0	2876	6 AR258505	AR258505 Sequence
16	556	100.0	2876	6 AR258511	AR258511 Sequence
17	556	100.0	2876	6 AR380642	AR380642 Sequence
18	556	100.0	2876	6 AX156115	AX156115 Sequence

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

19	556	100.0	2876	8 HUMPAI	M16006 Human plasm
20	556	100.0	2937	6 CQ861596	CQ861596 Sequence
21	556	100.0	2937	8 HUMPAIB	M14083 Human beta-
22	556	100.0	2944	6 I08667	I08667 Sequence 4
23	556	100.0	3171	6 AX281751	AX281751 Sequence
24	554.4	99.7	1209	11 AY891093	AY891093 Synthetic
25	554.4	99.7	1482	6 AX787059	AX787059 Sequence
26	554.4	99.7	1482	8 HSPAIR	X04439 Human mRNA
27	548	98.6	1187	6 CQ785751	CQ785751 Sequence
28	548	98.6	1187	6 CQ795516	CQ795516 Sequence
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31	459.6	82.7	844	4 AF508034	AF508034 Equus cab
32	455.2	81.9	3000	4 SSPAII	Y11347 S.scrofa mr
33	452	81.3	2970	4 MVPAIL	X58541 Mink mRNA f
34	447.6	80.5	548	4 AF074325	AF074325 Oryctolag
35	447.2	80.4	2970	4 BTPAII1MR	X16383 Bovine mRNA
36	421.6	75.8	3053	6 AX827499	AX827499 Sequence
37	421.6	75.8	3053	9 RAYPAIIA	M24067 Rattus norv
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42	359.8	64.7	9360	8 HSM809316	BM649164 Homo sapi
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44	204.2	36.7	249	4 BTPAII	X52906 Bovine PAI-
45	203.6	36.6	14544	6 CQ880126	CQ880126 Sequence

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
AY888695 1209 bp mRNA linear SYN 22-MAR-2005
Synthetic construct Homo sapiens clone FLH031026.01X serine or
cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
complete cds.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

Hines,L., Rolfs,A., Jepsen,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and Labaer,J.
Cloning of human full-length CDS in Creator (TM) recombinational
vector system
Unpublished
2 (bases 1 to 1209)
Hines,L., Rolfs,A., Jepsen,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and Labaer,J.
Direct Submission
Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge MA 02141, USA
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned with normalized stop-codon. The CDS
has been directionally cloned using BD In-Fusion(TM) cloning system
between the Sali and HindIII sites of the pDNR-Dual vector.
Additional sequences in the clone: 'ACC' after Sali site and
before 'ATG' to provide Kozak consensus sequence. Each clone is
clonally isolated and full-length sequence-verified.
Location/Qualifiers
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/db_xref="taxon:32630"
/clone="FLH031026.01X"

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1. 1209      /genes="SERPINE1"
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ORIGIN

Query Match	100.0%;	Score 556;	DB 11;	Length 1209;
Best Local Similarity	100.0%;	Pred. No. 5.1e-119;		
Matches 556;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AAGGAGCTCATGGGCGCATCGAAACAAGGATGAGATCAGACACACAGACGCGATCTTCGTC	60	
DB	307	AAGGAGCTCATGGGCGCATCGAAACAAGGATGAGATCAGACACACAGACGCGATCTTCGTC	366	
QY	61	CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCACTTCTTCAAGGTGTTCCGGAGC	120	
DB	367	CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCACTTCTTCAAGGTGTTCCGGAGC	426	
QY	121	ACGGTCAAGCAAGTGCATCTTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG	180	
DB	427	ACGGTCAAGCAAGTGCATCTTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG	486	
QY	181	GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTCTGGGAAAGAGCCGTGGACCCAG	240	
DB	487	GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTCTGGGAAAGAGCCGTGGACCCAG	546	
QY	241	CTGACACGGCTGTGTGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC	300	
DB	547	CTGACACGGCTGTGTGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC	606	
QY	301	CCGCACTCCAGCACCCACCGCCGCTCTTCCACAAATCAGACGGCAGCACTGCTCTGTG	360	
DB	607	CCGCACTCCAGCACCCACCGCCGCTCTTCCACAAATCAGACGGCAGCACTGCTCTGTG	666	
QY	361	CCCATGATGCTCAGACCCAAACAAGTTCAACTATCTAGTTTCCACGCCGATGCCCAT	420	
DB	667	CCCATGATGCTCAGACCCAAACAAGTTCAACTATCTAGTTTCCACGCCGATGCCCAT	726	
QY	421	TACTACGACATCCTGGAACTGGCCCTACCGGGGACACCTCAGCACTGTTCAATGCTGCC	480	
DB	727	TACTACGACATCCTGGAACTGGCCCTACCGGGGACACCTCAGCACTGTTCAATGCTGCC	786	
QY	481	CCTTATGAAAAAGAGGTGCCCTCTCTCTGCCCTCACCACAACTTCTGAGTGCCCAAGCTCATC	540	
DB	787	CCTTATGAAAAAGAGGTGCCCTCTCTCTGCCCTCACCACAACTTCTGAGTGCCCAAGCTCATC	846	
QY	541	AGCCACTGGAAAGGCA	556	
DB	847	AGCCACTGGAAAGGCA	862	

RESULT	2
AY889067	
LOCUS	
DEFINITION	AY889067 1209 bp mRNA linear SYN 29-MAR-2005
	Synthetic construct Homo sapiens clone FJH016840.OIX serine or

cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA, complete cds.

ACCESSION AY889067
VERSION
GI:60654586
KEYWORDS
Human ORF Project.
SOURCE
synthetic construct
ORGANISM
synthetic construct
other sequences: artificial sequences.

REFERENCE
AUTHORS
1 (bases 1 to 1209)
Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and Labaer, J.

TITLE Cloning of human full-length CDS in Creator (TM) recombinational vector system

JOURNAL
REFERENCE
Unpublished
2 (bases 1 to 1209)

2 (Lanes 1 to 12)
REFERENCES
Hines, L., Rolfs, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and LaBaer, J.

TITLE
Direct Submission
JOURNAL
Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA

COMMENT

This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector.

Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide korak consensus sequence. Each clone is clonally isolated and full-length sequence-verified.

FEATURES
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ORIGIN

Query Match	100.0%	Score 556;	DB 11;	Length 1209;
Best Local Similarity	100.0%;	Pred. NO. 5.1e-119;		
Matches 556:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	AAGAGGCTCATGGGGCCATGGAACAAGGATGAGATCAGACCAACAGACCGGATCTTCGTC	60
Db	307	AAGAGGCTCATGGGGCCATGGAACAAGGATGAGATCAGACCAACAGACCGGATCTTCGTC	366

Qy	61	CAGCGGATCTGAAGTGGTCAGGGCTTCATGCCCACTCTTTCAGGCTGTTCGGAGC	120
Db	367	CAGCGGATCTGAAGTGGTCAGGGCTTCATGCCCACTCTTTCAGGCTGTTCGGAGC	426
Qy	121	ACGGTCAAGCAAGTGACTTTTCAGAGTGGAGAGCCAGATCATCATCATGACTGG	180

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Db 427 ACAGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCATCATGCTGG 486
QY 181 GTGAAGACACACAAAAGGTATGATCAGCACTTGTGTTGGAAAGAGCGGTGGACCA 240
Db 487 GTGAAGACACACAAAAGGTATGATCAGCACTTGTGTTGGAAAGAGCGGTGGACCA 546
QY 241 CTGACACGGCTGTGCTGGTGAATGCTCTTACTTCAACGCCAGTGGAGACTCCCTTC 300
Db 547 CTGACACGGCTGTGCTGGTGAATGCTCTTACTTCAACGCCAGTGGAGACTCCCTTC 606
QY 301 CCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGCCAGCTGTCTGTG 360
Db 607 CCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGCCAGCTGTCTGTG 666
QY 361 CCATGATGCTGACACCAAGTTCAATATCTAGTTTCACTGAGTTCCACGCCAGTGGCCAT 420
Db 667 CCATGATGCTGACACCAAGTTCAATATCTAGTTTCACTGAGTTCCACGCCAGTGGCCAT 726
QY 421 TACTACGACATCTGGAACCTCCCTACCGGGGACACCTCAGCATGTTCTGTGCC 480
Db 727 TACTACGACATCTGGAACCTCCCTACCGGGGACACCTCAGCATGTTCTGTGCC 786
QY 481 CCTTATGAAAAGAGTGCCTCTCTGTGCGCTCACCACAACTTCTGAGTGCCAGCTCATC 540
Db 787 CCTTATGAAAAGAGTGCCTCTCTGTGCGCTCACCACAACTTCTGAGTGCCAGCTCATC 846
QY 541 AGCCACTGGAAGGCA 556
Db 847 AGCCACTGGAAGGCA 862
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RESULT 3

AY891356
LOCUS
DEFINITION
Synthetic construct Homo sapiens clone FLH031022.01L serine or
cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
partial cds.

ACCESSION
AY891356VERSION
AY891356.1KEYWORDS
Human ORF Project.SOURCE
synthetic constructORGANISM
synthetic constructREFERENCE
other sequences; artificial sequences.AUTHORS
1. (bases 1 to 1209)

Hines, L., Rolfs, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F.,

Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,

Williamson, J. and Labaer, J.

Cloning of human full-length CDS in Creator (TM) recombinational

vector system

Unpublished

JOURNAL
2. (bases 1 to 1209)

Hines, L., Rolfs, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F.,

Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,

Williamson, J. and Labaer, J.

Direct Submission

Submitted (05-JAN-2005) Biological Chemistry and Molecular

Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,

Cambridge, MA 02141, USA

This CDS clone is a part of a collection of human full-length

expression clones generated by Harvard Institute of Proteomics.

This ORF clone has been cloned without stop-codon (to allow fusion

with C-terminal tag). The CDS has been directionally cloned using

BD In-Fusion (TM) cloning system between the Sali and HindIII sites

of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'

after Sali site and before 'ATG' to provide Kozak consensus

sequence; 'GG' after last codon and before HindIII site to maintain

reading frame. Each clone is clonally isolated and full-length

sequence-verified.

Location/Qualifiers

1. .1209

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/mol_type="mRNA"

FEATURES

source

RESULT 4

AY891655

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1. .>1209
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ORIGIN

Query Match 100.0%; Score 556; DB 11; Length 1209;
Best Local Similarity 100.0%; Pred. No. 5,1e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGAGCTCATGGGGCCATGGAAAGGATGAGATCAGACACACAGCGGATCTTCGTC 60
Db 307 AAGGAGCTCATGGGGCCATGGAAAGGATGAGATCAGACACACAGCGGATCTTCGTC 366
QY 61 CAGCGGATCTGAAGCTGTTCAGGGCTTCATGCCCTCTTTCAGGGTGTTCGGAGC 120
Db 367 CAGCGGATCTGAAGCTGTTCAGGGCTTCATGCCCTCTTTCAGGGTGTTCGGAGC 426
QY 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 180
Db 427 ACGGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG 486
QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTCTTGGGAAAGAGCGGTGGACCA 240
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Db 547 CTGACACGGCTGTGCTGTGATGCCCTTCAACGGCCAGTGGAGACTCCCTTC 606
QY 301 CCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGCCAGCTGTCTGTG 360
Db 607 CCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGCCAGCTGTCTGTG 666
QY 361 CCATGATGCTCAGACCAACAAAGTTCAATATCTAGTTTCAACGCCCGGATGCCAT 420
Db 667 CCATGATGCTCAGACCAACAAAGTTCAATATCTAGTTTCAACGCCCGGATGCCAT 726
QY 421 TACTACGACATCTGGAAGTGCCTTACACGGGGACACCTCAGCATGTTCTGTGCC 480
Db 727 TACTACGACATCTGGAAGTGCCTTACACGGGGACACCTCAGCATGTTCTGTGCC 786
QY 481 CCTTATGAAAAGAGTGCCTCTCTGTGCGCTCACCACAACTTCTGAGTGCCAGCTCATC 540
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Db 847 AGCCACTGGAAGGCA 862

RESULT 4

AY891655

LOCUS AY891655. 1209 bp mRNA linear SYN 29-MAR-2005
 DEFINITION Synthetic construct Homo sapiens clone FLH016836.01L serine or cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA, partial cds.
 ACCESSION AY891655
 VERSION AY891655.1 GI:61370956
 KEYWORDS Human ORF Project.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 1209)
 AUTHORS Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.
 TITLE Cloning of human full-length CDS in Creator (TM) recombinational vector system
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1209)
 AUTHORS Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.
 TITLE Direct Submission
 JOURNAL Submitted (05-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
 COMMENT This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length sequence-verified.
 FEATURES
 Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
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 VLFMQQVMEPL"

ORIGIN

Query Match 100.0%; Score 556; DB 11; Length 1209;
 Best Local Similarity 100.0%; Pred. No. 5.1e-119;
 Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGGAGCTCATGGGCGCATGGAAACAGGATGATGATGAGTACGACACACAGCGCGATCTTCGTC 60
 Db 307 AAGGAGCTCATGGGCGCATGGAAACAGGATGATGATGAGTACGACACACAGCGCGATCTTCGTC 366
 QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 120

Db 367 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 426
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 Db 547 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606
 QY 301 CCCGACTCCAGCACCCACCGCGCGCTCTTCACAATCAGACGGCAGCACTGTCTCTGTG 360
 Db 607 CCCGACTCCAGCACCCACCGCGCGCTCTTCACAATCAGACGGCAGCACTGTCTCTGTG 666
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 Db 727 TACTACGACATCTCTGGAACTGCCCTTACCACGGGGACACCTCAGCATGTTCATTGCTGCC 786
 QY 481 CCTATGAAAAGAGGTGCTCTCTCGCTCCTCACCACATCTCAGTGCCTCCGAGTCCATC 540
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 QY 541 AGCCACTGGAAGGCA 556
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AY893400 1209 bp mRNA linear SYN 16-MAR-2005
 DEFINITION Synthetic construct Homo sapiens clone FLH057235.01X serine or cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA, complete cds.
 ACCESSION AY893400
 VERSION AY893400.1 GI:60817775
 KEYWORDS Human ORF Project.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 1209)
 AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.
 TITLE Cloning of human full-length CDS FLEXGene in Gateway(TM) recombinational vector system
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1209)
 AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
 COMMENT This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. AttB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence-verified.
 Location/Qualifiers
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 /organism="synthetic construct"

FEATURES

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from placenta and brain"
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LSAQLIHWKGNTRPRLILVLPKFSLETVEDLRLKPLENLGMDTMRFOQADFTSLSD
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ORIGIN

Query Match	100.0.0%;	Score 556;	DB 11;	Length 1209;
Best Local Similarity	100.0.0%;	Pred. No. 5.1e-119;		
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QY	1	AAGGAGCTCATGGGCGCATCGAAACAAGGATGAGATCAGCACACACGACGACGCGATCTTCGTC	60	
Db	307	AAGGAGCTCATGGGCGCATCGAAACAAGGATGAGATCAGCACACACGACGACGCGATCTTCGTC	366	
QY	61	CAGCGGGATCTGAAGCTGTGCTCCAGGGCTTCATGCCCCACTTCTTTCAGGCTGTGTTCCGGAGC	120	
Db	367	CAGCGGGATCTGAAGCTGTGCTCCAGGGCTTCATGCCCCACTTCTTTCAGGCTGTGTTCCGGAGC	426	
QY	121	ACGGTCAACGACAGTGCACATTTTTCAGAGGTGGAGAGCCAGGATTCATCATGACTGCTG	180	
Db	427	ACGGTCAACGACAGTGCACATTTTTCAGAGGTGGAGAGCCAGGATTCATCATGACTGCTG	486	
QY	181	GTGAAGACACACACAAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCCAG	240	
Db	487	GTGAAGACACACACAAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCCAG	546	
QY	241	CTGACACGGCTGTGCTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAGAAGCTCCCTTTC	300	
Db	547	CTGACACGGCTGTGCTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAGAAGCTCCCTTTC	606	
QY	301	CCCGACTCCAGCACCCACCGCCGCTCTTCCACAAATCAGACGGCAGCACTGCTCTGTG	360	
Db	607	CCCGACTCCAGCACCCACCGCCGCTCTTCCACAAATCAGACGGCAGCACTGCTCTGTG	666	
QY	361	CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACGGCCGATGGCCAT	420	
Db	667	CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACGGCCGATGGCCAT	726	
QY	421	TACTACGACATCTGGAATCGGCCTTACACGGGGACACCTCAGCATGTTTCAATGCTGCC	480	
Db	727	TACTACGACATCTGGAATCGGCCTTACACGGGGACACCTCAGCATGTTTCAATGCTGCC	786	
QY	481	CCTTATGAAAAAGAGTGCTCTCTCTGCGCTTCAACCAATTTCTAGTGGCCACAGCTCATC	540	
Db	787	CCTTATGAAAAAGAGTGCTCTCTCTGCGCTTCAACCAATTTCTAGTGGCCACAGCTCATC	846	
QY	541	AGCCACTGGAAGGGCA	556	
Db	847	AGCCACTGGAAGGGCA	862	

RESULT 6

AY893851 1209 bp mRNA linear SYN 16-MAR-2005
 LOCUS
 DEFINITION Synthetic construct Homo sapiens clone FLH057231.01L serine or
 cysteine proteinase inhibitor clade E member 1 (SERPINE1) mRNA,
 partial cds.
 ACCESSION AY893851
 VERSION AY893851.1 GI:60829666
 KEYWORDS Human ORF Project.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 1209)
 AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,
 Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
 TITLE Cloning of human full-length CDS FLEXGene in
 Gateway(TM)recombinational vector system
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1209)
 AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,
 Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JAN-2005) Biological Chemistry and Molecular
 Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
 Cambridge, MA 02141, USA
 COMMENT This CDS clone is a part of a collection of human full-length
 expression clones generated by Harvard Institute of Proteomics.
 This ORF clone has been cloned without stop-codon (to allow fusion
 with C-terminal tag). AtB recombination sites have been added to
 either end of the ORF and directionally cloned using the Gateway
 cloning system into pDONR 201. Additional sequences in the clone:
 'ACC' before the 'ATG' (corresponding to ribosomal binding site and
 Kozak consensus sequences). Each clone is clonally isolated and
 full-length sequence-verified.
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 from placenta and brain"
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 gene
 CDS

ORIGIN

Query Match	100.0%	Score 556;	DB 11;	Length 1209;
Best Local Similarity	100.0%	Pred. No. 5.1e-119;		
Matches 556;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	AAGGAGCTATGGGGCCATGGAAACAGGATGAGATCAGCACACAGACGGATCTTCGTC	60
Dd	307	AAGGAGCTATGGGGCCATGGAAACAGGATGAGATCAGCACACAGACGGATCTTCGTC	366
QY	61	CAGCGGGATCTGAAGCTTGGTCTCAGGGGCTTCATGCCCCACTTCTTCAGGCTGTTCGGGAGC	120

367	DB	CAGCGG	ATCTGA	AGCTGGTCCAGG	GCTTCATG	CCCCACTCTTCTCAGG	CTGTTCGG	AGC	426
121	QY	ACGGTCA	AGCAAGTGG	ACTTTTCAGAG	TGGAGAGCCAG	ATTCATCAT	CAATGAC	TGG	180
427	DB	ACGGTCA	AGCAAGTGG	ACTTTTCAGAG	TGGAGAGCCAG	ATTCATCAT	CAATGAC	TGG	486
181	QY	GTGAAG	CACACACAAA	AGGTATGATCAG	CAACTTCTG	TGGAAA	AGGAGCCGTG	GACCA	240
487	DB	GTGAAG	CACACACAAA	AGGTATGATCAG	CAACTTCTG	TGGAAA	AGGAGCCGTG	GACCA	546
241	QY	CTGAC	CAGGCTGGT	CTGGTGAATCC	CTCTACTTTCA	ACGGCCAGTGG	AAGACTCC	CTTTC	300
547	DB	CTGAC	CAGGCTGGT	CTGGTGAATCC	CTCTACTTTCA	ACGGCCAGTGG	AAGACTCC	CTTTC	606
301	QY	CCCGACT	CCAGACCC	ACCGCGCTCTTCC	CAAAATCAG	ACGGCAGCA	CTGTCTCTG	TG	360
607	DB	CCCGACT	CCAGACCC	ACCGCGCTCTTCC	CAAAATCAG	ACGGCAGCA	CTGTCTCTG	TG	666
361	QY	CCCATG	TGGTCTCAG	ACCAACAAAGT	TTCAACTATCTG	AGTTTCA	CCACGCCCCG	ATGGCCAT	420
667	DB	CCCATG	TGGTCTCAG	ACCAACAAAGT	TTCAACTATCTG	AGTTTCA	CCACGCCCCG	ATGGCCAT	726
421	QY	TACTAC	GACATCTTGG	AATCGCCCTAC	ACGCGGGA	CACCTCAG	CAGATTTCA	TTCGTG	480
727	DB	TACTAC	GACATCTTGG	AATCGCCCTAC	ACGCGGGA	CACCTCAG	CAGATTTCA	TTCGTG	786
481	QY	CTTTATG	AAAAAGAGT	GCCTCTCTCTG	CCCTTCA	CCAACTTCTCAG	TGCGCCAG	CTCATC	540
787	DB	CTTTATG	AAAAAGAGT	GCCTCTCTCTG	CCCTTCA	CCAACTTCTCAG	TGCGCCAG	CTCATC	846
541	QY	AGCC	ACTGG	AAAGGCA	556				
847	DB	AGCC	ACTGG	AAAGGCA	862				

RESULT 7	CQ716284	1532 bp	DNA	linear	PAT 03-FEB-2000
LOCUS	CQ716284				
DEFINITION	Sequence 2218 from Patent WO02068579.				
ACCESSION	CQ716284				
VERSION	CQ716284.1	GI:42277141			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.				
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof				
JOURNAL	Patent: WO 02068579-A 2218 06-SEP-2002;				
PE Corporation (NY) (US)					
LOCATION/Qualifiers					
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Best Local Similarity	100.0%;	Pred. No. 5.1e-119;			
Matches 556;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Qy	61	CAGCGGATCTGAAGCTGGTCCAGGGCTTTCAGCCCACTTCTTCAGGCTGTTCCGGAGC	120		
Db	513	CAGCGGATCTGAAGCTGGTCCAGGGCTTTCAGCCCACTTCTTCAGGCTGTTCCGGAGC	572		

QY	121	ACGGTCAAGCAAGTGGACCTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG	180
Db	573	ACGGTCAAGCAAGTGGACCTTTTCAGAGGTGGAGAGCCAGATTCATCATCAATGACTGG	632
QY	181	GTGAAGACACACAAAAGCTATGATCAGCAACTTCTTGGGAAAGAGCGCTGGACCAG	240
Db	633	GTGAAGACACACAAAAGGTATGATCAGCAACTTCTTGGGAAAGAGCGCTGGACCAG	692
QY	241	CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGATCCTCCTTC	300
Db	693	CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGATCCTCCTTC	752
QY	301	CCGACTCCAGACCCACCGCGCCTCTTCCACAAATCAGACGGCAGCATGTCTCTGTG	360
Db	753	CCGACTCCAGACCCACCGCGCCTCTTCCACAAATCAGACGGCAGCATGTCTCTGTG	812
QY	361	CCCATGATGCTCAGACCAACAGTTCAACTATCTAGTTTACCAGCCCGATGGCCAT	420
Db	813	CCCATGATGCTCAGACCAACAGTTCAACTATCTAGTTTACCAGCCCGATGGCCAT	872
QY	421	TACTACGACATCTCGAACTGCCCTACACGGGACACCCCTCAGCATGTTTCATTGTGCC	480
Db	873	TACTACGACATCTCGAACTGCCCTACACGGGACACCCCTCAGCATGTTTCATTGTGCC	932
QY	481	CTTTATGAAAAGAGGTCCTCTCTCTGCCCCCTCACCACCAATCTCGAGTCCCCAGCTCATC	540
Db	933	CTTTATGAAAAGAGGTCCTCTCTCTGCCCCCTCACCACCAATCTCGAGTCCCCAGCTCATC	992
QY	541	AGCCACTGGAAAGGCA 556	
Db	993	AGCCACTGGAAAGGCA 1008	
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HSPAIR1			
LOCUS	Human mRNA for plasminogen activator inhibitor (PAI-1). linear PRI 27-MAR-1995		
DEFINITION	HSPAIR1		
ACCESSION	X04744.1		
VERSION	X04744.1 GI:35275		
KEYWORDS	glycoprotein; plasminogen activator inhibitor.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1962)		
AUTHORS	Wun,T.-C. and Kretzmer,K.K.		
TITLE	cDNA cloning and expression in E. coli of a plasminogen activator inhibitor (PAI) related to a PAI produced by Hep G2 hepatoma cell		
JOURNAL	FEBS Lett. 210 (1), 11-16 (1987)		
PUBMED	3026837		
COMMENT	Data kindly reviewed (20-AUG-1987) by Wun T.-C.		
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Query Match      100.0%; Score 556; DB 8; Length 1962;
Best Local Similarity 100.0%; Pred. No. 5,1e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 379 ACGGTCAAGCAAGTGGATCTTTTCAGAGGTGGAGAGCCAGATTCATCAATCAATGCTGG 438

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QY 361 CCATGATGCTCAGACCAACAAAGTTCAATATATGAGTTCAACCGCCGATGGCCAT 420
Db 619 CCATGATGCTCAGACCAACAAAGTTCAATATATGAGTTCAACCGCCGATGGCCAT 678

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QY 481 CTTTATGAAAAGAGGTGCTCTCTCTGCGCTCACCACATCTGAGTCCCGAGCTCATC 540
Db 739 CTTTATGAAAAGAGGTGCTCTCTCTGCGCTCACCACATCTGAGTCCCGAGCTCATC 798

QY 541 AGCCACTGAAAAGGCA 556
Db 799 AGCCACTGAAAAGGCA 814

RESULT 9
BC010860
LOCUS
DEFINITION
Homo sapiens serine (or cysteine) proteinase inhibitor, clade E
(nexin, plasminogen activator inhibitor type 1), member 1, mRNA
(CDNA clone MGC:9226 IMAGE:3893914), complete cds.
ACCESSION
BC010860
VERSION
BC010860.1 GI:14790035
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 2207)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toehiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McSwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2207)

NIH MGC Project
Direct Submission
Submitted (12-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAC Plate: 14 Row: 9 Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 10835158.

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TVSPVMAQTNKFNTEFTTPDGHYDILELPHGDTLSMFIAPYKEVPLSALTNI
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ORIGIN
Query Match 100.0%; Score 556; DB 8; Length 2207;
Best Local Similarity 100.0%; Pred. No. 5.1e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCCCATGGAACAGGATGAGATCAGCACACAGACCGCATCTTCGTC 60
DB 429 AAGGAGCTCATGGGCCCATGGAACAGGATGAGATCAGCACACAGACCGCATCTTCGTC 488
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTCTTCAGGCTGTTCGGAGC 120
DB 489 CAGCGGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTCTTCAGGCTGTTCGGAGC 548
QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 180
DB 549 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 608
QY 181 GTGAAGACACACAAAAGGTATGATCAGCACTTGTGGAAAAGGAGCCGTGGACAG 240
DB 609 GTGAAGACACACAAAAGGTATGATCAGCACTTGTGGAAAAGGAGCCGTGGACAG 668
QY 241 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGGCAGTGGAAAGTCCCTTC 300
DB 669 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGGCAGTGGAAAGTCCCTTC 728
QY 301 CCCGACTCCAGACCCACCGCCCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 360
DB 729 CCCGACTCCAGACCCACCGCCCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 788
QY 361 CCCATGATGGCTCAGACCAAGTTCACACTACTGATGTTACACGCCCGATGCCAT 420
DB 789 CCCATGATGGCTCAGACCAAGTTCACACTACTGATGTTACACGCCCGATGCCAT 848
QY 421 TACTACGACATCTCGAACTGGCTTACACGGGGACACCTCAGCATGTTCAATTCCTGCC 480
DB 849 TACTACGACATCTCGAACTGGCTTACACGGGGACACCTCAGCATGTTCAATTCCTGCC 908
QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCCCCCACCACAACTTCTGAGTGCCCGAGCTCATC 540
DB 909 CTTTATGAAAAGAGTGCTCTCTCTGCCCCCACCACAACTTCTGAGTGCCCGAGCTCATC 968
QY 541 AGCCACTGGAAGGCA 556
DB 969 AGCCACTGGAAGGCA 984

RESULT 10
LOCUS CQ413075 2660 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 20146 from Patent WO0170979.
ACCESSION CQ413075
VERSION CQ413075.1 GI:41320856
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lee,J. and Lillie,J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 20146 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 556; DB 6; Length 2660;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCCCATGGAACAGGATGAGATCAGCACACAGACCGCATCTTCGTC 60
DB 452 AAGGAGCTCATGGGCCCATGGAACAGGATGAGATCAGCACACAGACCGCATCTTCGTC 511
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTCTTCAGGCTGTTCGGAGC 120
DB 512 CAGCGGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTCTTCAGGCTGTTCGGAGC 571
QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 180
DB 572 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 631
QY 181 GTGAAGACACACAAAAGGTATGATCAGCACTTGTGGAAAAGGAGCCGTGGACAG 240
DB 632 GTGAAGACACACAAAAGGTATGATCAGCACTTGTGGAAAAGGAGCCGTGGACAG 691
QY 241 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGTCCCTTC 300
DB 692 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGTCCCTTC 751
QY 301 CCCGACTCCAGACCCACCGCCCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 360
DB 752 CCCGACTCCAGACCCACCGCCCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 811
QY 361 CCCATGATGGCTCAGACCAAGTTCACACTACTGATGTTACACGCCCGATGCCAT 420
DB 812 CCCATGATGGCTCAGACCAAGTTCACACTACTGATGTTACACGCCCGATGCCAT 871
QY 421 TACTACGACATCTCGAACTGGCTTACACGGGGACACCTCAGCATGTTCAATTCCTGCC 480
DB 872 TACTACGACATCTCGAACTGGCTTACACGGGGACACCTCAGCATGTTCAATTCCTGCC 931
QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCCCCCACCACAACTTCTGAGTGCCCGAGCTCATC 540
DB 932 CTTTATGAAAAGAGTGCTCTCTCTGCCCCCACCACAACTTCTGAGTGCCCGAGCTCATC 991
QY 541 AGCCACTGGAAGGCA 556
DB 992 AGCCACTGGAAGGCA 1007

RESULT 11
LOCUS AR106060 2876 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6103498.
ACCESSION AR106060
VERSION AR106060.1 GI:12820125
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2876)
AUTHORS Lawrence,D.A. and Stefansson,S.P.
TITLE Mutant plasminogen activator-inhibitor type 1 (PAI-1) and uses thereof
JOURNAL Patent: US 6103498-A 1 15-AUG-2000;
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ORIGIN
Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAAGATGAGATCAGACACAGACGCGATCTTCGTC 60
Db 382 AAGGAGCTCATGGGGCCATGGAAACAAGATGAGATCAGACACAGACGCGATCTTCGTC 441
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
Db 442 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 501
QY 121 ACGGTCAAGCAAGTGGATCTTTTTCAGAGGTGGAGAGGAGGAGGATTCATCATGACTGG 180
Db 502 ACGGTCAAGCAAGTGGATCTTTTTCAGAGGTGGAGAGGAGGAGGATTCATCATGACTGG 561
QY 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAGCGGTGGACCCAG 240
Db 562 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAGCGGTGGACCCAG 621
QY 241 CTGACACGGCTGTGTGGTGAATGCCCTTCTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 622 CTGACACGGCTGTGTGGTGAATGCCCTTCTTCAACGGCCAGTGGAAAGACTCCCTTC 681
QY 301 CCCGACTCCAGCACCCACCGCCGCTTCTTCCAAATCAGACGGGAGCACTGTCTGTG 360
Db 682 CCCGACTCCAGCACCCACCGCCGCTTCTTCCAAATCAGACGGGAGCACTGTCTGTG 741
QY 361 CCCATGATGCTCAGACCAACAAAGTTCAACTATCTAGTGTTCACCAACCGCCGATGCCAT 420
Db 742 CCCATGATGCTCAGACCAACAAAGTTCAACTATCTAGTGTTCACCAACCGCCGATGCCAT 801
QY 421 TACTAGACATCTCGAATCGCTTACCACGGGGACACCCCTCAGCATGTTTCATTGTGTC 480
Db 802 TACTAGACATCTCGAATCGCTTACCACGGGGACACCCCTCAGCATGTTTCATTGTGTC 861
QY 481 CTTTATGAAAAGAGGTGCTCTCTGCGCCCTCACCACCAATCTGAGTGCCCAAGCTCATC 540
Db 862 CTTTATGAAAAGAGGTGCTCTCTGCGCCCTCACCACCAATCTGAGTGCCCAAGCTCATC 921
QY 541 AGCCACTGGAAAGGCA 556
Db 922 AGCCACTGGAAAGGCA 937
RESULT 12
AR106066/c
LOCUS AR106066 2876 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 10 from patent US 6103498.
ACCESSION AR106066
VERSION AR106066.1 GI:12820131
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2876)
AUTHORS Lawrence, D.A. and Stefansson, S.P.
TITLE Mutant plasminogen activator-inhibitor type 1 (PAI-1) and uses thereof
JOURNAL Patent: US 6103498-A 10 15-AUG-2000;
FEATURES
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ORIGIN
Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGGCCATGGAAACAAGATGAGATCAGACACAGACGCGATCTTCGTC 60
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QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
Db 2435 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 2376

QY 121 ACGGTCAAGCAAGTGGATCTTTTTCAGAGGTGGAGAGGAGGAGGATTCATCATGACTGG 180
Db 2375 ACGGTCAAGCAAGTGGATCTTTTTCAGAGGTGGAGAGGAGGAGGATTCATCATGACTGG 2316
QY 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAGCGGTGGACCCAG 240
Db 2315 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAGCGGTGGACCCAG 2256
QY 241 CTGACACGGCTGTGTGGTGAATGCCCTTCTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 2255 CTGACACGGCTGTGTGGTGAATGCCCTTCTTCAACGGCCAGTGGAAAGACTCCCTTC 2196
QY 301 CCCGACTCCAGCACCCACCGCCGCTTCTTCCAAATCAGACGGGAGCACTGTCTGTG 360
Db 2195 CCCGACTCCAGCACCCACCGCCGCTTCTTCCAAATCAGACGGGAGCACTGTCTGTG 2136
QY 361 CCCATGATGCTCAGACCAACAAAGTTCAACTATCTAGTGTTCACCAACCGCCGATGCCAT 420
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QY 421 TACTAGACATCTCGAATCGCTTACCACGGGGACACCCCTCAGCATGTTTCATTGTGTC 480
Db 2075 TACTAGACATCTCGAATCGCTTACCACGGGGACACCCCTCAGCATGTTTCATTGTGTC 2016
QY 481 CTTTATGAAAAGAGGTGCTCTCTGCGCCCTCACCACCAATCTGAGTGCCCAAGCTCATC 540
Db 2015 CTTTATGAAAAGAGGTGCTCTCTGCGCCCTCACCACCAATCTGAGTGCCCAAGCTCATC 1956
QY 541 AGCCACTGGAAAGGCA 556
Db 1955 AGCCACTGGAAAGGCA 1940
RESULT 13
BD094083
LOCUS BD094083 2876 bp DNA linear PAT 27-AUG-2002
DEFINITION Shear stress-responsive DNAs.
ACCESSION BD094083
VERSION BD094083.1 GI:22639671
KEYWORDS WO 0125427-A/44.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2876)
AUTHORS Nojima, H., Yoshisue, H., Obayashi, M., Ota, T., Kawabata, A., Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.
TITLE Shear stress-responsive DNAs
JOURNAL Patent: WO 0125427-A 44 12-APR-2001;
KYOWA HAKKO KOGYO CO LTD, HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, AVAKO KAWABATA, KAZUHIRO SAKURADA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA, SUMIO SUGANO
COMMENT OS Homo sapiens (human)
PN WO 0125427-A/44
PD 12-APR-2001
PF 02-OCT-2000 WO 2000JP006840
PR 01-OCT-1999 JP 99P 280976
PI HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, PI AVAKO KAWABATA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA, KAZUHIRO SAKURADA, TETSURO KUGA, SUMIO SUGANO
PI C12N15/12, C07K14/435, C07K16/18, C12P21/02, C12Q1/68, A61K38/00, A61K39/395
PC A61K48/00, A61P9/10, G01N33/50, G01N33/53
CC
FH Key Location/Qualifiers
FT CDS (76)..(1281).
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Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCCATGGAAACAAAGATGAGATCAGCACACAGACGCGATCTTCGTC 60
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Db 382 AAGGAGCTCATGGGCCATGGAAACAAAGATGAGATCAGCACACAGACGCGATCTTCGTC 441

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 120
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Db 442 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 501

QY 121 ACGGTCGAAGCTGGTTCAGAGGTGAGAGCCAGATTCAATCAATGACTGG 180
    |||||
Db 502 ACGGTCGAAGCTGGTTCAGAGGTGAGAGCCAGATTCAATCAATGACTGG 561

QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCGGTGGACCG 240
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Db 562 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCGGTGGACCG 621

QY 241 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGAAGACTCCCTTC 300
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Db 622 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGAAGACTCCCTTC 681

QY 301 CCGGACTCCAGCACCCAGCGCGCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 360
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Db 682 CCGGACTCCAGCACCCAGCGCGCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 741

QY 361 CCCATGATGGCTCAGACCAAGTTCACTATCTAGATTCAACACGCCGATGGCCAT 420
    |||||
Db 742 CCCATGATGGCTCAGACCAAGTTCACTATCTAGATTCAACACGCCGATGGCCAT 801

QY 421 TACTACGACATCCTGGAATCGCTTACCACGGGGACACCCCTCAGCATGTTCAATGCTGCC 480
    |||||
Db 802 TACTACGACATCCTGGAATCGCTTACCACGGGGACACCCCTCAGCATGTTCAATGCTGCC 861

QY 481 CCTTATGAAAAGAGGTGCTCTCTGCGCTTCCACCAATCTAGTGGCCAGCTCATC 540
    |||||
Db 862 CCTTATGAAAAGAGGTGCTCTCTGCGCTTCCACCAATCTAGTGGCCAGCTCATC 921

QY 541 AGCCACTGGAAGGCA 556
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Db 922 AGCCACTGGAAGGCA 937

RESULT 14
LOCUS      CQ776713          2876 bp      DNA      linear      PAT 11-MAR-2004
DEFINITION Sequence 399 from Patent EP1394274.
ACCESSION  CQ776713.1
VERSION    CQ776713.1
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuwara,K.
TITLE      Methods of testing for bronchial asthma or chronic obstructive
JOURNAL    Pulmonary disease
PATENT     EP 1394274-A 399 03-MAR-2004;
Genox Research, Inc. (JP)
LOCATION/Qualifiers
FEATURES   source
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ORIGIN
Query Match      100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCCATGGAAACAAAGATGAGATCAGCACACAGACGCGATCTTCGTC 60
    |||||
Db 382 AAGGAGCTCATGGGCCATGGAAACAAAGATGAGATCAGCACACAGACGCGATCTTCGTC 441

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 120
    |||||
Db 442 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 501

QY 121 ACGGTCGAAGCTGGTTCAGAGGTGAGAGCCAGATTCAATCAATGACTGG 180
    |||||
Db 502 ACGGTCGAAGCTGGTTCAGAGGTGAGAGCCAGATTCAATCAATGACTGG 561

QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCGGTGGACCG 240
    |||||
Db 562 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCGGTGGACCG 621

QY 241 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGAAGACTCCCTTC 300
    |||||
Db 622 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGAAGACTCCCTTC 681

QY 301 CCGGACTCCAGCACCCAGCGCGCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 360
    |||||
Db 682 CCGGACTCCAGCACCCAGCGCGCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 741

QY 361 CCCATGATGGCTCAGACCAAGTTCACTATCTAGATTCAACACGCCGATGGCCAT 420
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Db 742 CCCATGATGGCTCAGACCAAGTTCACTATCTAGATTCAACACGCCGATGGCCAT 801

QY 421 TACTACGACATCCTGGAATCGCTTACCACGGGGACACCCCTCAGCATGTTCAATGCTGCC 480
    |||||
Db 802 TACTACGACATCCTGGAATCGCTTACCACGGGGACACCCCTCAGCATGTTCAATGCTGCC 861

QY 481 CCTTATGAAAAGAGGTGCTCTCTGCGCTTCCACCAATCTAGTGGCCAGCTCATC 540
    |||||
Db 862 CCTTATGAAAAGAGGTGCTCTCTGCGCTTCCACCAATCTAGTGGCCAGCTCATC 921

QY 541 AGCCACTGGAAGGCA 556
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Db 922 AGCCACTGGAAGGCA 937

RESULT 15
LOCUS      AR258505          2876 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6489143.
ACCESSION  AR258505
VERSION    AR258505.1
KEYWORDS   Unknwon.
SOURCE     Unknwon.
ORGANISM   Unknwon.
REFERENCE  1 (bases 1 to 2876)
AUTHORS    Lawrence,D.A. and Stefansson,S.P.
TITLE      Mutant plasminogen activator-inhibitor type 1 (PAI-1) proteins
JOURNAL    Patent: US 6489143-A 1 03-DEC-2002;
American National Red Cross; Falls Church, VA
LOCATION/Qualifiers
FEATURES   source
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ORIGIN
Query Match      100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCCATGGAAACAAAGATGAGATCAGCACACAGACGCGATCTTCGTC 60
    |||||
Db 382 AAGGAGCTCATGGGCCATGGAAACAAAGATGAGATCAGCACACAGACGCGATCTTCGTC 441
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Query Match      100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCCATGGAAACAAAGATGAGATCAGCACACAGACGCGATCTTCGTC 60
    |||||
Db 382 AAGGAGCTCATGGGCCATGGAAACAAAGATGAGATCAGCACACAGACGCGATCTTCGTC 441

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 120
    |||||
Db 442 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 501

QY 121 ACGGTCGAAGCTGGTTCAGAGGTGAGAGCCAGATTCAATCAATGACTGG 180
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Db 502 ACGGTCGAAGCTGGTTCAGAGGTGAGAGCCAGATTCAATCAATGACTGG 561

QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCGGTGGACCG 240
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    |||||
Db 622 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGAAGACTCCCTTC 681

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    |||||
Db 682 CCGGACTCCAGCACCCAGCGCGCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 741

QY 361 CCCATGATGGCTCAGACCAAGTTCACTATCTAGATTCAACACGCCGATGGCCAT 420
    |||||
Db 742 CCCATGATGGCTCAGACCAAGTTCACTATCTAGATTCAACACGCCGATGGCCAT 801

QY 421 TACTACGACATCCTGGAATCGCTTACCACGGGGACACCCCTCAGCATGTTCAATGCTGCC 480
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Db 802 TACTACGACATCCTGGAATCGCTTACCACGGGGACACCCCTCAGCATGTTCAATGCTGCC 861

QY 481 CCTTATGAAAAGAGGTGCTCTCTGCGCTTCCACCAATCTAGTGGCCAGCTCATC 540
    |||||
Db 862 CCTTATGAAAAGAGGTGCTCTCTGCGCTTCCACCAATCTAGTGGCCAGCTCATC 921

QY 541 AGCCACTGGAAGGCA 556
    |||||
Db 922 AGCCACTGGAAGGCA 937

RESULT 15
LOCUS      AR258505          2876 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6489143.
ACCESSION  AR258505
VERSION    AR258505.1
KEYWORDS   Unknwon.
SOURCE     Unknwon.
ORGANISM   Unknwon.
REFERENCE  1 (bases 1 to 2876)
AUTHORS    Lawrence,D.A. and Stefansson,S.P.
TITLE      Mutant plasminogen activator-inhibitor type 1 (PAI-1) proteins
JOURNAL    Patent: US 6489143-A 1 03-DEC-2002;
American National Red Cross; Falls Church, VA
LOCATION/Qualifiers
FEATURES   source
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ORIGIN
Query Match      100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 5e-119;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCCATGGAAACAAAGATGAGATCAGCACACAGACGCGATCTTCGTC 60
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Db 382 AAGGAGCTCATGGGCCATGGAAACAAAGATGAGATCAGCACACAGACGCGATCTTCGTC 441
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Qy 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120
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Qy 442 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 501
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Qy 121 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTTCATCAATGACTGG 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 502 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTTCATCAATGACTGG 561
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Qy 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTGTTGGAAAGAGCGGTGGACCAG 240
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Qy 562 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTGTTGGAAAGAGCGGTGGACCAG 621
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Qy 241 CTGACAGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
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Qy 622 CTGACAGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 681
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Qy 301 CCCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 360
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Qy 682 CCCGACTCCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 741
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 CCCATGATGGTCAAGCAAGTTCAACTATATCTAGTTTCAACGCCCGATGGCCAT 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 742 CCCATGATGGTCAAGCAAGTTCAACTATATCTAGTTTCAACGCCCGATGGCCAT 801
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 421 TACTACGACATCCTGGAACTGCCCTACACGGGGACACCCCTCAGCATGTTCAITGTGCC 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 802 TACTACGACATCCTGGAACTGCCCTACACGGGGACACCCCTCAGCATGTTCAITGTGCC 861
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 CCTTATGAAAAGAGGTGCCTCTCTGCGCTCACCACCAATTCCTGAGTGGCCAGCTCATC 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 862 CCTTATGAAAAGAGGTGCCTCTCTGCGCTCACCACCAATTCCTGAGTGGCCAGCTCATC 921
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 AGCCACTGGAAAGGCA 556
Db |||||||||||||||
Qy 922 AGCCACTGGAAAGGCA 937
Db |||||||||||||||
```

Search completed: March 10, 2006, 01:01:12
Job time : 3287 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 22:55:30 ; Search time 471.5 Seconds
(without alignments)
7859.107 Million cell updates/sec

Title: US-10-686-428A-4_COPY_238_793

Perfect score: 556

Sequence: 1 aaggagctcatgggcatg.....catcagccactggaagga 556

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq 21.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	1209	10	Adf28770 Human pla
2	556	100.0	1209	10	Aad64654 Human pla
3	556	100.0	1209	10	Adv42563 Human psy
4	556	100.0	1209	14	Aea81050 Human pla
5	556	100.0	1962	10	Acf79499 Human pla
6	556	100.0	2016	13	Acn41744 Human dia
7	556	100.0	2053	13	Acn41743 Human dia
8	556	100.0	2177	14	Adv70121 Tumor-ass
9	556	100.0	2660	5	Adl61934 Human ova
10	556	100.0	2870	6	Abv94750 Human pan
11	556	100.0	2876	2	Aat97303 Human pla
12	556	100.0	2876	4	Aas09460 Human cdn
13	556	100.0	2876	4	Aah02917 Human she
14	556	100.0	2876	6	Abv77991 Hypoxia-r
15	556	100.0	2876	10	Acf79498 Human pla
16	556	100.0	2876	10	Aad64644 Human pla
17	556	100.0	2876	11	Adi31861 Human cdn
18	556	100.0	2876	11	Adn95545 Human bec
19	556	100.0	2876	12	Adj75147 Marker ge

20	556	100.0	2876	12	Adl35811	Adl35811 Human pla
21	556	100.0	2876	13	Acn38690	Acn38690 Tumour-as
22	556	100.0	2876	13	Adp23373	Adp23373 PRO polyyp
23	556	100.0	2876	13	AdS83928	AdS83928 Human lym
24	556	100.0	2876	14	Aea81038	Aea81038 Human pla
25	556	100.0	2876	14	Aeb29660	Aeb29660 Human Ser
26	556	100.0	2937	13	AdS52878	AdS52878 Drug ther
27	556	100.0	2944	1	AAH80253	AAH80253 Insert of
28	556	100.0	3171	6	AA894905	AA894905 Human DNA
29	556	100.0	3172	8	ABX63842	ABX63842 Human CDN
30	556	100.0	3172	10	ADJ56200	ADJ56200 Human CDN
31	555.6	100.0	2876	10	ADe48114	ADe48114 Human PAI
32	555	99.8	2876	9	ACF06144	ACF06144 Human pla
33	554.4	99.7	1482	10	AA056136	AA056136 Human pla
34	554.4	99.7	2132	2	AAQ06594	AAQ06594 Clone ECE
35	553.6	99.6	2899	13	ADQ38428	ADQ38428 Human SNP
36	553.6	99.6	3320	13	ADQ38429	ADQ38429 Human SNP
37	548	98.6	1187	12	ADM41307	ADM41307 Human pla
38	541.6	97.4	1482	1	AAH81524	AAH81524 Complete
39	452	81.3	2370	10	ACF79500	ACF79500 Mink plas
40	447.2	80.4	2970	10	ACF79497	ACF79497 Cattle pl
41	421.6	75.8	3053	10	ACF79503	ACF79503 Rat plasm
42	421.6	75.8	3053	10	AA064653	AA064653 Rat plasm
43	421.6	75.8	3053	10	ABT41815	ABT41815 Toxicity
44	421.6	75.8	3053	11	ADW21854	ADW21854 Rat hepat
45	421.6	75.8	3053	12	ADP72654	ADP72654 Renal tox

ALIGNMENTS

RESULT 1

ADP28770

ID ADF28770 standard; cdna; 1209 BP.

XX

AC ADF28770;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human plasminogen-activator inhibitor-1 (PAI-1) encoding cDNA.

XX

Urokinase-type plasminogen activator; uPA;

plasminogen-activator inhibitor-1; PAI-1; breast cancer; tumour;

KW

cancer therapy; human; ss; gene.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

FT CDS

1..1209

/tag= a

/product= "PAI-1"

/note= "plasminogen activator inhibitor type 1"

FT

FT

XX

WO2003082072-A2.

XX

PD 09-OCT-2003.

XX

13-FEB-2003; 2003WO-US0004538.

XX

13-FEB-2002; 2002US-0356928P.

PR

09-AUG-2002; 2002US-0402311P.

XX

(HARB/) HARBECK N.

(KATE/) KATES R E.

(SCHM/) SCHMITT M.

(FOEK/) FOEKENS J A.

PI

Harbeck N, Kates RE, Schmitt M, Foekens JA;

DR

WPI; 2003-803930/75.

XX

P-PSDB; ADF28771.

XX

Selecting treatments for cancer, specifically breast cancer, based on

PT levels of urokinase and plasminogen-activator inhibitor-1 in tissue.
XX Disclosure; SEQ ID NO 3; 133pp; English.
XX
XX
CC The invention relates to selecting a treatment regime with highest
CC expected benefit to a patient with primary breast cancer. The method
CC involves measuring the levels of urokinase-type plasminogen activator
CC (uPA) and plasminogen-activator inhibitor-1 (PAI-1), or corresponding
CC mRNA, in primary tumour tissue (or a sample); and classifying the patient
CC as low risk (LR) if the uPA level is below a cut-off value of between the
CC 55 th . and 75 th percentile of normalized or analogous uPA in a
CC randomized population of breast cancer patients, and if the PAI-1 level
CC is lower than a cut-off value between the 61 st and 81 st percentile in
CC the same population, or as high risk (HR) if the levels of uPA and PAI-1
CC are above these cut-off values. The treatment of LR (or HR) patients is
CC then selected as one that results in the highest expected benefit in a
CC comparable population of LR (or HR) patients. The method is used: for
CC selection of the most effective therapy, including one designed to
CC prevent relapse; and to predict expected benefit, overall or disease-free
CC survival in patients with cancer, particularly of the breast but also
CC leukemia and plasmacytoma. The method can also be used: to predict the
CC benefit of preventative treatment for relapse of cancer, especially where
CC HR patients are treated with bisphosphonate drugs; for deciding whether
CC or not to administer an aggressive or non-aggressive regime; and for
CC deciding whether or not to administer chemotherapy in combination with
CC hormone therapy (i.e. if the patient is LR, chemotherapy is not
CC administered; in this case HR patients are those who are estrogen- and/or
CC progesterone- receptor positive). The present sequence represents a cDNA
CC encoding a human PAI-1 polypeptide.
XX

Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 10; Length 1209;
Best Local Similarity 100.0%; Pred. No. 5e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAGGATGAGATCAGCACACAGACCGCATCTTCGTC 60
DB 307 AAGGAGCTCATGGGGCCATGGAAACAGGATGAGATCAGCACACAGACCGCATCTTCGTC 366

QY 61 CAGCGGGATCTGAAGCTGGTCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120
DB 367 CAGCGGGATCTGAAGCTGGTCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 426

QY 121 ACGGTCACGAGTGGCTTTTCAGAGTGGAGAGCCAGATTCATCATCAATGACTGG 180
DB 427 ACGGTCACGAGTGGCTTTTCAGAGTGGAGAGCCAGATTCATCATCAATGACTGG 486

QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCCGTGACCCAG 240
DB 487 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCCGTGACCCAG 546

QY 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGAAGACTCCCTTC 300
DB 547 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGAAGACTCCCTTC 606

QY 301 CCCGACTCCAGCACCCAGCCGCTCTTCCAAATCAGAGCGGAGCAGCTGTCTCTGG 360
DB 607 CCCGACTCCAGCACCCAGCCGCTCTTCCAAATCAGAGCGGAGCAGCTGTCTCTGG 666

QY 361 CCCATGAGGCTCAGACCAACAAAGTTCAACTATCTAGATTCCACCACGCCGATGCCAT 420
DB 667 CCCATGAGGCTCAGACCAACAAAGTTCAACTATCTAGATTCCACCACGCCGATGCCAT 726

QY 421 TACTACGATCTCTGGAACTGCCCTACACCGGGACACCTCAGCATGTTCAATGCTGCC 480
DB 727 TACTACGATCTCTGGAACTGCCCTACACCGGGACACCTCAGCATGTTCAATGCTGCC 786

QY 481 CTTTATGAAAGAGTGCCTCTCTGCTCCCTCACCACATCTCAGTGCCTCAGCTCATC 540
DB 787 CTTTATGAAAGAGTGCCTCTCTGCTCCCTCACCACATCTCAGTGCCTCAGCTCATC 846

QY 541 AGCCACTGGAAAGGCA 556

DB 847 AGCCACTGGAAAGGCA 862

RESULT 2
AAD64654
ID AAD64654 standard; cDNA; 1209 BP.
XX
AC AAD64654;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human plasminogen activator inhibitor-1 (PAI-1) coding region.
XX
KW Plasminogen activator inhibitor-1; PAI-1; cardiovascular disease;
KW fibrotic disease; gene therapy; antiinflammatory; gene; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..1209
FT /*tag= a
FT /product= "Human plasminogen activator inhibitor-1
FT protein"
FT /note= "Capital T represents cleavage sites"
XX
PN US2003199463-A1.
XX
PD 23-OCT-2003.
XX
PF 23-APR-2002; 2002US-00128706.
XX
PR 23-APR-2002; 2002US-00128706.
XX
PA (ITES/) ITESCU S.
XX
PI Itescu S;
XX
DR WPI; 2003-852809/79.
DR P-PSDB; ABW02690.
XX
PT New catalytic nucleic acid that hybridizes to and specifically cleaves an
PT mRNA encoding a Plasminogen Activator Inhibitor-1, useful in preparing a
PT composition for treating e.g., cardiovascular or fibrotic disease.
XX
PS Disclosure; SEQ ID NO 17; Opp; English.
XX
CC The present invention relates to a new catalytic nucleic acid that
CC hybridizes to and specifically cleaves an mRNA encoding a plasminogen
CC activator inhibitor-1 (PAI-1). The invention is useful in preparing a
CC composition for treating cardiovascular or fibrotic disease. The
CC invention is also used in gene therapy. The present sequence is human
CC plasminogen activator inhibitor-1 (PAI-1) coding region
XX
SQ Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 10; Length 1209;
Best Local Similarity 100.0%; Pred. No. 5e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAGGATGAGATCAGCACACAGACCGCATCTTCGTC 60
DB 307 AAGGAGCTCATGGGGCCATGGAAACAGGATGAGATCAGCACACAGACCGCATCTTCGTC 366

QY 61 CAGCGGGATCTGAAGCTGGTCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120
DB 367 CAGCGGGATCTGAAGCTGGTCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 426

QY 121 ACGGTCACGAGTGGCTTTTCAGAGTGGAGAGCCAGATTCATCATCAATGACTGG 180
DB 427 ACGGTCACGAGTGGCTTTTCAGAGTGGAGAGCCAGATTCATCATCAATGACTGG 486

QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCCGTGACCCAG 240

Db 487 GTGAAGACACACAAAGGATGATCAGCAACTTCTTGGAAAGGAGCGGTGGACCAG 546
QY 241 CTGACACGGCTGGTGGTGAATGCGCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 547 CTGACACGGCTGGTGGTGAATGCGCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606
QY 301 CCCGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCACTGCTCTGTG 360
Db 607 CCCGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCACTGCTCTGTG 666
QY 361 CCCATGATGCTCAGACCAAGTTCACACTATCTAGTTCACCAAGCCGCGGATGGCCAT 420
Db 667 CCCATGATGCTCAGACCAAGTTCACACTATCTAGTTCACCAAGCCGCGGATGGCCAT 726
QY 421 TACTAGACATCTGGAACTGCGCTTACCAGGGGACACCTCAGCATGTTTCATGTCGCC 480
Db 727 TACTAGACATCTGGAACTGCGCTTACCAGGGGACACCTCAGCATGTTTCATGTCGCC 786
QY 481 CCTTATGAAAGAGGTGCGCTCTCTGCGCTTACCAGGGGACACCTCAGCATGTTTCATGTCGCC 540
Db 787 CCTTATGAAAGAGGTGCGCTCTCTGCGCTTACCAGGGGACACCTCAGCATGTTTCATGTCGCC 846
QY 541 AGCCACTGGAAAGGCA 556
Db 847 AGCCACTGGAAAGGCA 862
RESULT 3
ADV42563
ID ADV42563 standard; cdna; 1209 BP.
XX
AC ADV42563;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrine immune expressed sequence tag SEQ ID NO 191.
XX
KW microarray; psychoneuroendocrine immune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004WO-US017686.
XX
PR 04-JUN-2003; 2003US-0475915P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nicholson A, Vernon SD;
XX
DR WPI; 2005-031682/03.
XX
PT New microarray comprising probes for genes involved in
PT psychoneuroendocrine immune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 191; 254pp; English.
XX
CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrine immune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrine immune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.

XX
SQ Sequence 1209 BP; 275 A; 374 C; 316 G; 244 T; 0 U; 0 Other;
Query Match 100.0%; Score 556; DB 14; Length 1209;
Best Local Similarity 100.0%; Pred. No. 5e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGAGCTCATGGGGCCATGGAAACAAGGATGAGATCAGACCAACGAGCGATCTTCGTC 60
Db 307 AGGAGCTCATGGGGCCATGGAAACAAGGATGAGATCAGACCAACGAGCGATCTTCGTC 366
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
Db 367 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 426
QY 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG 180
Db 427 ACGGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTCATCAATGACTGG 486
QY 181 GTGAAGACACACAAAGGATGATCAGCAACTTCTTGGGAAAGGAGCGGTGGACCAG 240
Db 487 GTGAAGACACACAAAGGATGATCAGCAACTTCTTGGGAAAGGAGCGGTGGACCAG 546
QY 241 CTGACACGGCTGGTGGTGAATGCGCTTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 547 CTGACACGGCTGGTGGTGAATGCGCTTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606
QY 301 CCCGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCACTGCTCTGTG 360
Db 607 CCCGACTCCAGCACCCACCGCGCTCTTCCAAATCAGACGGCAGCACTGCTCTGTG 666
QY 361 CCCATGATGCTCAGACCAAGTTCACACTATCTAGTTCACCAAGCCGCGGATGGCCAT 420
Db 667 CCCATGATGCTCAGACCAAGTTCACACTATCTAGTTCACCAAGCCGCGGATGGCCAT 726
QY 421 TACTAGACATCTGGAACTGCGCTTACCAGGGGACACCTCAGCATGTTTCATGTCGCC 480
Db 727 TACTAGACATCTGGAACTGCGCTTACCAGGGGACACCTCAGCATGTTTCATGTCGCC 786
QY 481 CCTTATGAAAGAGGTGCGCTCTCTGCGCTTACCAGGGGACACCTCAGCATGTTTCATGTCGCC 540
Db 787 CCTTATGAAAGAGGTGCGCTCTCTGCGCTTACCAGGGGACACCTCAGCATGTTTCATGTCGCC 846
QY 541 AGCCACTGGAAAGGCA 556
Db 847 AGCCACTGGAAAGGCA 862
RESULT 4
AEA81050
ID AEA81050 standard; cdna; 1209 BP.
XX
AC AEA81050;
XX
DT 08-SEP-2005 (first entry)
XX
DE Human plasminogen activator inhibitor-1 encoding cDNA SEQ ID NO:17.
XX
KW antisense therapy; RNA interference; plasminogen activator inhibitor-1;
KW vasotropic; thrombolytic; hemostatic; vascular disease;
KW thrombocyte disorder; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1209
FT /tag= a
FT /product= "plasminogen activator inhibitor-1 (PAI-1)"
PN US2005148527-A1.
XX
PD 07-JUL-2005.
XX

CC improvement of a vascular thrombotic disorder, asthma, chronic
CC obstructive pulmonary disease, alopecia, undesired weight loss such as
CC anorexia, Alzheimer's disease, systemic amyloid deposition, systemic
CC amyloidosis, myelofibrosis, glomerulosclerosis, male pattern baldness,
CC keloids, apocrine cysts, acne, atherosclerosis, ageing,
CC hepatosplenomegaly, extramedullary haematopoiesis, or a wound (claimed)
XX
SQ Sequence 1962 BP; 456 A; 569 C; 505 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 10; Length 1962;
Best Local Similarity 100.0%; Pred. No. 5.8e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGGCTCATGGGGCCATGGAAACAGGATGAGATCAGCACCAGACGGAGCTTCGTC 60
DB |||||
QY 259 AAGAGGCTCATGGGGCCATGGAAACAGGATGAGATCAGCACCAGACGGAGCTTCGTC 318
DB |||||
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTTCAGGCTGTTCCGGAGC 120
DB |||||
QY 319 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTTCAGGCTGTTCCGGAGC 378
DB |||||
QY 121 ACGGTCAAGCAAGTGGATTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGCTG 180
DB |||||
QY 379 ACGGTCAAGCAAGTGGATTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGCTG 438
DB |||||
QY 181 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCGGTGGACCCAG 240
DB |||||
QY 439 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCGGTGGACCCAG 498
DB |||||
QY 241 CTGACAGGCTGGTGGTGGTGAATGCTCTACTTCAACGGCCAGTGGAAAGATCCCTTC 300
DB |||||
QY 499 CTGACAGGCTGGTGGTGGTGAATGCTCTACTTCAACGGCCAGTGGAAAGATCCCTTC 558
DB |||||
QY 301 CCGACTCCAGACCCACCCCGGCTCTTCCAAATCAGACGGCAGCATGTCTCTGTG 360
DB |||||
QY 559 CCGACTCCAGACCCACCCCGGCTCTTCCAAATCAGACGGCAGCATGTCTCTGTG 618
DB |||||
QY 361 CCATGATGCTCAGACCAAGTTCACATCTACTGATTTACCGCCGAGTGGCCAT 420
DB |||||
QY 619 CCATGATGCTCAGACCAAGTTCACATCTACTGATTTACCGCCGAGTGGCCAT 678
DB |||||
QY 421 TACTAGCAGATCTGGAACCTGACCCAGCGGACACCTCTAGCATGTTCTATTGCTGCC 480
DB |||||
QY 679 TACTAGCAGATCTGGAACCTGACCCAGCGGACACCTCTAGCATGTTCTATTGCTGCC 738
DB |||||
QY 481 CTTATGAAAGAGTGGCTCTCTGCTGCTTCCCAATTCAGATGAGTGGCCAGCTCATC 540
DB |||||
QY 739 CTTATGAAAGAGTGGCTCTCTGCTGCTTCCCAATTCAGATGAGTGGCCAGCTCATC 798
DB |||||
QY 541 AGCCACTGGGAAGGCA 556
DB |||||
QY 799 AGCCACTGGGAAGGCA 814
DB |||||

RESULT 6
ACN41744
ID ACN41744 standard; cDNA; 2016 BP.
XX
AC ACN41744;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:619.
XX
KW ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
XX dittp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX

PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Garstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LJ;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;
PI Xu Y, Kwong M, Pollock JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
WPI; 2004-329368/30.
P-PSDB; ABM83092.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 1; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dittp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dittp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dittp polynucleotide of
CC the invention. Note: The sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 2016 BP; 464 A; 628 C; 508 G; 416 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 13; Length 2016;
Best Local Similarity 100.0%; Pred. No. 5.8e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGCTCATGGGGCCATGGAAACAGGATGAGATCAGCACCAGACGGAGCTTCGTC 60
DB |||||
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTTCAGGCTGTTCCGGAGC 120
DB |||||
QY 489 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTTCAGGCTGTTCCGGAGC 548
DB |||||
QY 121 ACGGTCAAGCAAGTGGATTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGCTG 180
DB |||||
QY 549 ACGGTCAAGCAAGTGGATTTTCAGAGTGGAGAGCCAGATTCATCAATCAATGCTG 608
DB |||||
QY 181 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGCTGGACCCAG 240
DB |||||
QY 609 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGCTGGACCCAG 668
DB |||||
QY 241 CTGACAGGCTGGTGGTGAATGCTCTCTCACTTCAACGGCCAGTGGAAAGATCCCTTC 300
DB |||||
QY 669 CTGACAGGCTGGTGGTGAATGCTCTCTCACTTCAACGGCCAGTGGAAAGATCCCTTC 728
DB |||||
QY 301 CCGGACTCCAGACCCAGCCGCTCTTCCAAATCAGAGCGGAGCATGCTCTCTGTG 360
DB |||||
QY 729 CCGGACTCCAGACCCAGCCGCTCTTCCAAATCAGAGCGGAGCATGCTCTCTGTG 788
DB |||||

XX 23-MAY-2003; 2003US-0473238P.
PR 27-FEB-2004; 2004US-0548299P.
XX (GETH) GENENTECH INC.
PA Phillips H;
XX WPI; 2005-048766/05.
DR P-PSDB; ADV70216.
XX Treating a mammal having a tumor of glial origin comprising cells that
PT express a type A or B glial tumor antigen by contacting the cells with a
PT composition comprising first and second binding agents.
XX Disclosure; SEQ ID NO 45; 374pp; English.
XX
XX The invention describes a method of treating a mammal having a tumor of
CC glial origin comprising cells that express a type A or B glial tumor
CC antigen comprising contacting the cells with a composition of: a first
CC binding agent comprising a first antibody, oligopeptide or organic
CC molecule that binds to a type A or B glial tumor antigen; and a second
CC binding agent comprising a second antibody, oligopeptide or organic
CC molecule that binds to a type B or A glial tumor antigen. Also described
CC is a method of determining the presence of a type A or B glial tumor in a
CC mammal. The method is useful in treating a mammal having a tumor of glial
CC origin comprising cells that express a type A or B glial tumor antigen.
CC This sequence represents a human tumor-associated antigenic target
CC polynucleotide.
XX
SQ Sequence 2177 BP; 515 A; 638 C; 553 G; 471 T; 0 U; 0 Other;
Query Match 100.0%; Score 556; DB 14; Length 2177;
Best Local Similarity 100.0%; Pred. No. 6e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCATGGAACAAGGATGAGATCAGACACACACGCGATCTTCGTC 60
DB 414 AAGGAGCTCATGGGCGCATGGAACAAGGATGAGATCAGACACACACGCGATCTTCGTC 473
QY 61 CAGCGGGATCTGAAGCTGGTTCAGAGGCTTCATGCCCCACTTCTTCAGGCTGTTCGGAGC 120
DB 474 CAGCGGGATCTGAAGCTGGTTCAGAGGCTTCATGCCCCACTTCTTCAGGCTGTTCGGAGC 533
QY 121 AGGTCACGAGTGAATCTTCAGAGGCTGGAGAGGCGAGATTCATCATCATGACTGG 180
DB 534 AGGTCACGAGTGAATCTTCAGAGGCTGGAGAGGCGAGATTCATCATCATGACTGG 593
QY 181 GTGACACACACACAAAGATGATCAGCACTTCTTGGGAAAGGCGGTGGACACG 240
DB 594 GTGACACACACACAAAGATGATCAGCACTTCTTGGGAAAGGCGGTGGACACG 653
QY 241 CTGACACGCGTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
DB 654 CTGACACGCGTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 713
QY 301 CCGGACTCCAGCACCCACCGCGGCTCTTCCAAATCAGACGGCAGCAGTGTCTGTG 360
DB 714 CCGGACTCCAGCACCCACCGCGGCTCTTCCAAATCAGACGGCAGCAGTGTCTGTG 773
QY 361 CCCATGATGGCTCAGACCAACAGTTCATCTATCTAGTTCACACGCCCGATGCCAT 420
DB 774 CCCATGATGGCTCAGACCAACAGTTCATCTATCTAGTTCACACGCCCGATGCCAT 833
QY 421 TACTACGATCTCGGAATCGCCCTACACGGGGACACCCCTCAGCATGTTTCATGTCG 480
DB 834 TACTACGATCTCGGAATCGCCCTACACGGGGACACCCCTCAGCATGTTTCATGTCG 893
QY 481 CTTTATGAAAAAGAGTGCTCTCTCTGCGCTTCCAAACATCTAGTGTCCAGCTCATC 540
DB 894 CTTTATGAAAAAGAGTGCTCTCTCTGCGCTTCCAAACATCTAGTGTCCAGCTCATC 953
QY 541 AGCCACTGGAAAGGCA 556

DB 954 AGCCACTGGAAAGGCA 969
RESULT 9
ADL61934
ID ADL61934 standard; DNA; 2660 BP.
XX
AC ADL61934;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #20146.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 20146; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the

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CC invention.
XX SQ Sequence 2660 BP; 615 A; 799 C; 653 G; 593 T; 0 U; 0 Other;

Query Match
Best Local Similarity 100.0%; Score 556; DB 5; Length 2660;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAGGATGATCAGCAACACAGAGCGCGATCTTCGTC 60
DB 452 AAGGAGCTCATGGGGCCATGGAAACAGGATGATCAGCAACACAGAGCGCGATCTTCGTC 511

QY 61 CAGCGGATCTGAAGCTGGTCCAGGCTTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120
DB 512 CAGCGGATCTGAAGCTGGTCCAGGCTTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 571

QY 121 ACGGTCAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTTCATCAATCAATGACTGG 180
DB 572 ACGGTCAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTTCATCAATCAATGACTGG 631

QY 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGCTGGACCA 240
DB 632 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGCTGGACCA 691

QY 241 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
DB 692 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 751

QY 301 CCGGACTCCAGCACCCAGCGCGCTCTTCCAAATCAGCGGAGCACTGTCTCTGTG 360
DB 752 CCGGACTCCAGCACCCAGCGCGCTCTTCCAAATCAGCGGAGCACTGTCTCTGTG 811

QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACCGCCGATGCCAT 420
DB 812 CCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACCGCCGATGCCAT 871

QY 421 TACTACGACATCCTGGAACTGCCCTTACCAACGGGGACACCCCTCAGCATGTTCTGTC 480
DB 872 TACTACGACATCCTGGAACTGCCCTTACCAACGGGGACACCCCTCAGCATGTTCTGTC 931

QY 481 CTTTATGAAAAGAGTGCTCTCTGCGCTCAGCAATCTTGAATGTCGCCAGCTCATC 540
DB 932 CTTTATGAAAAGAGTGCTCTCTGCGCTCAGCAATCTTGAATGTCGCCAGCTCATC 591

QY 541 AGCCACTGGAAAGGCA 556
DB 992 AGCCACTGGAAAGGCA 1007

RESULT 10
ID ABV94750
XX ABV94750 standard; cDNA; 2870 BP.
AC ABV94750;
XX
DT 14-JAN-2003 (first entry)
DE Human pancreatic cancer expressed cDNA SEQ ID NO 131.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
```

21-MAR-2001; 2001US-0278651P.
28-APR-2001; 2001US-0287112P.
16-MAY-2001; 2001US-0291631P.
12-JUL-2001; 2001US-0305484P.
20-AUG-2001; 2001US-0313999P.
27-NOV-2001; 2001US-0333626P.
(CORI-) CORIXA CORP.

Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
WPI; 2002-627435/67.
P-PSDB; ABP68605.

New isolated polynucleotide and pancreatic tumor polypeptides, useful for
diagnosing, preventing and/or treating cancer, particularly pancreatic
cancer.

Claim 1; SEQ ID NO 131; 300pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (I) comprising: (a)
any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
complements of (a); (c) sequences consisting of at least 20 contiguous
residues of (a); (d) sequences that hybridize to (a), under moderately
stringent conditions; (e) sequences having at least 75% or 90% identity
to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
in a patient and compositions comprising polypeptides, polynucleotides,
antibodies, fusion proteins, T cell populations and antigen presenting
cells expressing the polypeptide are useful in treating pancreatic cancer
and stimulating an immune response. The polynucleotides can be used as
probes or primers for nucleic acid hybridisation, in the design and
preparation of ribozyme molecules for inhibiting expression of the tumour
polypeptides and proteins in the tumour cells, in vaccines and for gene
therapy. Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 2870 BP; 704 A; 792 C; 725 G; 649 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 6; Length 2870;
Best Local Similarity 100.0%; Pred. No. 6.5e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAGGATGATCAGCAACACAGAGCGCGATCTTCGTC 60
DB 376 AAGGAGCTCATGGGGCCATGGAAACAGGATGATCAGCAACACAGAGCGCGATCTTCGTC 435

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120
DB 436 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 495

QY 121 ACGGTCAGCAAGTGGACTTTTCAGAGTGGAGAGCGCAATTCATCAATCAATGACTGG 180
DB 496 ACGGTCAGCAAGTGGACTTTTCAGAGTGGAGAGCGCAATTCATCAATCAATGACTGG 555

QY 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGCTGGACCA 240
DB 556 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGCTGGACCA 615

QY 241 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
DB 616 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 675

QY 301 CCGGACTCCAGACCCAGCGCGCTTTCACAAATCAGAGCGGAGCACTGTCTCTGTG 360
DB 676 CCGGACTCCAGACCCAGCGCGCTTTCACAAATCAGAGCGGAGCACTGTCTCTGTG 735

QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACCGCCGATGCCAT 420
DB 736 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACCGCCGATGCCAT 795

QY 421 TACTACGACATCCTGGAACTGCCCTTACCAACGGGGACACCCCTCAGCATGTTCTGTC 480


```
FT mat_peptide /note= "Both forms of the protein are detected in vivo"  
FT 144..1281 /*tag= e  
FT /label= Mature_PAI_1 #2  
FT /note= "Both forms of the protein are detected in vivo"  
XX  
PN WO200138560-A2.  
XX  
XX 31-MAY-2001.  
XX  
XX 22-NOV-2000; 2000WO-US032315.  
XX  
XX 22-NOV-1999; 99US-0167553P.  
XX  
XX (AMNA-) AMERICAN NAT RED CROSS.  
XX  
XX Lawrence DA, Day D;  
XX  
XX WPI; 2001-441438/47.  
DR P-PSDB; AAU04913.  
XX  
XX Detecting a functionally active form of an enzyme in a biological sample  
XX comprises contacting an enzyme inhibitor immobilized on a solid  
XX substrate.  
XX  
XX Disclosure; Fig 3; 69pp; English.  
XX  
XX The sequence encodes human plasminogen activator inhibitor-1, PAI-1, a  
XX serine proteinase inhibitor or serpin. The protein is used to demonstrate  
XX the method of the invention which comprises detecting a functionally  
XX active form of an enzyme in a biological sample by contacting an enzyme  
XX inhibitor immobilised on a solid substrate with the biological sample and  
XX measuring the binding of the enzyme inhibitor to the active form of the  
XX enzyme by a detectable label, where the enzyme inhibitor specifically  
XX forms a covalent bond or binds with a dissociation constant of 1 x 10-9M  
XX or less with the active form of the enzyme. The present invention  
XX provides a sensitive method for the detection of a functionally active  
XX form of an enzyme in a biological sample. Human PAI-1 can be used to  
XX detect a number of enzymes including tissue plasminogen activator,  
XX urokinase, thrombin, plasmin, neutrophil elastase, pancreatic elastase,  
XX trypsin, chymotrypsin, cathepsin G and prostate specific antigen and as  
XX such can be used in methods to diagnose diseases such as cystic fibrosis,  
XX acute respiratory distress syndrome (ARDS), HIV infection, TNF-mediated  
XX inflammation, prostate cancer and benign prostatic hypertrophy  
XX  
XX Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 556; DB 4; Length 2876;  
Best Local Similarity 100.0%; Pred. No. 6.5e-137;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGGAGCTCATGGGCCCATGGACAGGATGAGATCAGACCCACAGCGCGATCTTCGTC 60  
DB 382 AAGGAGCTCATGGGCCCATGGACAGGATGAGATCAGACCCACAGCGCGATCTTCGTC 441  
QY 61 CAGCGGGATCTGAAGTGTGTGTCAGGGCTTCATGCCCTTCCTTCAGGCTGTTCGGAGC 120  
DB 442 CAGCGGGATCTGAAGTGTGTGTCAGGGCTTCATGCCCTTCCTTCAGGCTGTTCGGAGC 501  
QY 121 ACGGTCAAGCAAGTGAGCTTTTCAGAGTGGAGAGCGCAGATTTCATCATCAATCACTGG 180  
DB 502 ACGGTCAAGCAAGTGAGCTTTTCAGAGTGGAGAGCGCAGATTTCATCATCAATCACTGG 561  
QY 181 GTGAGACACACACAAAGGATGATCAGCACTTGTCTTGGAAAGGAGCGGTGACACAG 240  
DB 562 GTGAGACACACACAAAGGATGATCAGCACTTGTCTTGGAAAGGAGCGGTGACACAG 621  
QY 241 CTGACACGGCTGGTGTGTAATGCCCTTCTACTTCAACGGCGCAGTGAAGACTCCCTTC 300  
DB 622 CTGACACGGCTGGTGTGTAATGCCCTTCTACTTCAACGGCGCAGTGAAGACTCCCTTC 681  
QY 301 CCCGACTCAGACCCACCGCCGCTCTTTTCCAAATCAGACGGCAGCACTGTCTCTGTG 360  
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DB 682 CCGGACTCCAGACCCACCGCGGCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 741  
QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTAGTGTTCACCAACCGCGATGCCCAT 420  
DB 742 CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTAGTGTTCACCAACCGCGATGCCCAT 801  
QY 421 TACTACGACATCTCTGGAACTGCCCTTACCAACGGGAGACCCCTCAGCATGTTTCAATGCTGCC 480  
DB 802 TACTACGACATCTCTGGAACTGCCCTTACCAACGGGAGACCCCTCAGCATGTTTCAATGCTGCC 861  
QY 481 CCTTATGAAAAGAGGTGCTCTCTGCGCCCTCACCACATCTCTGAGTGGCCAGCTCATC 540  
DB 862 CCTTATGAAAAGAGGTGCTCTCTGCGCCCTCACCACATCTCTGAGTGGCCAGCTCATC 921  
QY 541 AGCCACTGAAAAGGCA 556  
DB 922 AGCCACTGAAAAGGCA 937  
RESULT 13  
AAH02917  
ID AAH02917 standard; DNA; 2876 BP.  
XX  
XX AAH02917;  
AC  
XX 15-JUN-2001 (first entry)  
DT  
XX  
XX Human shear stress-response coding sequence SEQ ID NO: 87.  
DE  
XX Human; shear stress-response protein; vascular disease; arteriosclerosis;  
KW ds.  
XX  
XX Homo sapiens.  
OS  
XX WO200125427-A1.  
FN  
XX  
XX 12-APR-2001.  
PD  
XX  
XX 02-OCT-2000; 2000WO-JP006840.  
PF  
XX  
XX 01-OCT-1999; 99JP-00280976.  
PR  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
PA (NOJII/) NOJIMA H.  
PA  
XX  
XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;  
PI Kuga T, Sekine S, Nakamura Y, Sugano S;  
PI  
XX  
XX WPI; 2001-266308/27.  
DR P-PSDB; AAB90794.  
DR  
XX  
XX DNA sequences, proteins encoded by them and antibodies against them  
PT useful in diagnosis and treatment of vascular disease caused by  
PT arteriosclerosis.  
PT  
XX  
XX Claim 20; Page 472-476; 678pp; Japanese.  
PS  
XX  
XX The present invention provides the protein and coding sequences of a  
CC number of human shear stress response proteins. These are useful in the  
CC diagnosis, treatment and screening of vascular diseases caused by  
CC arteriosclerosis, including heart failure, post-PTCA restenosis and  
CC hypertension  
CC  
XX  
SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;  
Query Match 100.0%; Score 556; DB 4; Length 2876;  
Best Local Similarity 100.0%; Pred. No. 6.5e-137;  
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGGAGCTCATGGGCCCATGGACAGGATGAGATCAGACCCACAGCGCGATCTTCGTC 60  
DB 382 AAGGAGCTCATGGGCCCATGGACAGGATGAGATCAGACCCACAGCGCGATCTTCGTC 441
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Qy	61	CAGCGGATCTGAAGCTGGTTCAGGGCTTCATGCCCACTTCTTAGGCTGTTCCGGAGC	120
Db	442	CAGCGGATCTGAAGCTGGTTCAGGGCTTCATGCCCACTTCTTAGGCTGTTCCGGAGC	501
Qy	121	ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTATCATCAATGACTGG	180
Db	502	ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTATCATCAATGACTGG	561
Qy	181	GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTCTTGGAAAAGGAGCCGTGGACCAG	240
Db	562	GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTCTTGGAAAAGGAGCCGTGGACCAG	621
Qy	241	CTGACACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGAAGTCCCTTTC	300
Db	622	CTGACACGGCTGGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGAAGTCCCTTTC	681
Qy	301	CCCGACTCCAGACCCACCGCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG	360
Db	682	CCCGACTCCAGACCCACCGCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG	741
Qy	361	CCCATGATGGCTCAGACCAACAAAGTTTCAACTATACTGAGTTTCACCACGCCCGATGSCCAT	420
Db	742	CCCATGATGGCTCAGACCAACAAAGTTTCAACTATACTGAGTTTCACCACGCCCGATGSCCAT	801
Qy	421	TACTACGACATCTCGGAAGTCCCTTACCACGGGGACACCCCTCAGCATGTTCAATGCTGCC	480
Db	802	TACTACGACATCTCGGAAGTCCCTTACCACGGGGACACCCCTCAGCATGTTCAATGCTGCC	861
Qy	481	CTTTATGAAAAAGAGGTGCCTCTCTCTGCCCTTCAACCAATTCGTAGTGCCAGTCTATC	540
Db	862	CTTTATGAAAAAGAGGTGCCTCTCTCTGCCCTTCAACCAATTCGTAGTGCCAGTCTATC	921
Qy	541	AGCCACTGGAAAGGCA	556
Db	922	AGCCACTGGAAAGGCA	937

RESULT 14

ABV77991
ID ABV77991 standard; DNA; 2876 BP.

XX ABV77991:

DT 12-NOV-2002 (first entry)

DE Hypoxia-regulated protein coding sequence #11.

Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnery; gynecological; ophthalmological; vaccine; KW
KW
hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer; KW
ischaemic condition; reperfusion injury; retinopathy; neonatal stress; KW
preclampsia; atherosclerosis; inflammatory condition; wound healing; KW
inflammation; erythropliosis; hair loss; human; gene; ds. KW

OS Homo sapiens.

AA
PN
WO200246465-A2.

PD 13-JUN-2002.

10-DEC-2001; 2001WO-GB005458.

PR 08-DEC-2000; 2000GB-00030076.

FK 08-FEB-2001; 2001GB-00003156.
PR 25-OCT-2001; 2001GB-00025666.

PA (OXFO-) OXFORD BIOMEDICA UK LTD.

White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
PI
PI
PI
Rayner WN;

WPI; 2002-627238/67.

RESULT 15

PT Identifying a gene involved in disease for treating hypoxia-regulated
PT conditions, comprises comparing the transcriptome/proteome of two cell
PT types under different conditions and identifying a differentially
PT regulated gene.

PS Claim 37; Page 338; 538pp; English.

The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV77873-ABV78116 and ABP65061-ABP65237 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumorigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss

Sequence 2876 BP: 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 6; Length 2876;

Best Local Similarity 100.0%; Pred. No. 6.5e-137;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGAGCTCATGGGCCATGGAACAAGGATGAGATCAGCACACAGACGGATCTTCGTC 60

Db
382 AAGGAGCTCATGGGCCATGGAACAAGGATGAGATCAGCACACAGACGGATCTTCGTC 441

QY
61 CAGCGGATCTGAAGCTGGTCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120

Db 442 CAGCGGATCTGAAGCTGGTCAGGGCTTCATGCCCCACTTCTTCAGGCTGTTCGGAGC 501

QY 121 ACGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTTCATCATCAATGACTGG 180

Db 502 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTTCATCATCAATGACTGG 561

QY 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGCTTGGAAAGGAGCCGTGGACCAG 240

Db 562 GTGAAGACACACACAAAGTATGATCAGCAACTTGCTTGGAAAGAGCCGTGGACCAG 621

QY 241 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAGACTCCCTTC 300

Db 622 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAGACTCCCCCTC 681

QY 301 CCGACTCCAGCACCCACCGCGCCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 360

Db 682 CCCGACTCCAGCACCCACCGCGCCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTG 741

QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTATACTAGTTCACCACGCCGATGGCCAT 420

D_b 742 CCCATGATGGCTCAGACCAACAAGTTCAACTATACTAGTTCACCGCCGATGGCCAT 801

QY 421 TACTACGACATCCTGGAAGTGCCTACACGGGGACACCCCTCAGCATGTTCAATGCTGCC 480

Db 802 TACTACGACATCCTGGAACTGCCCTACACGGGGACACCCCTCAGCATGTTCATGTGCTGCC 861

QY 481 CCTTATGAAAAGAGGTGCTCTCTCTGCCCTCACCAACATTCTGAGTGCCAGCTCATC 540

Db 862 CCTATGAAAAGAGGTGCCTCTCTCTGCCCTCACCAACATTTCTGAGTGCCAGCTCATC 921

Qy 541 AGCCACTGGAAGGCA 556

Db 922 AGCCACTGGAAGGCA 937

ACF79498

ID ACF79498 standard; cDNA; 2876 BP.

XX AC ACF79498;

XX DT 18-DEC-2003 (first entry)

XX DE Human plasminogen activator inhibitor-1 cDNA.

XX KW Plasminogen activator inhibitor-1; PAI-1; human; transgenic;
XX KW thrombolytic; antiasthmatic; antiinflammatory; nootropic;
XX KW neuroprotective; antidepressant; nephrotropic; vulnerary;
XX KW antiaseborrheic; dermatological; antiarteriosclerotic; hepatotropic;
XX KW gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 76..1284
XX FT /*tag= a
XX FT /product= "Human PAI-1"

XX PN WO2003071267-A1.

XX PD 28-AUG-2003.

XX PF 19-FEB-2003; 2003WO-US005008.

XX PR 19-FEB-2002; 2002US-0358061P.

XX PA (UYVA-) UNIV VANDERBILT.

XX PP (DECL/) DECLERCK P J.

XX PI Déclerck PJ, Vaughan DE, Eren M;

XX WPI; 2003-721694/68.

XX DR P-PSDB; ABR63123.

XX PT Treating a warm-blooded vertebrate animal having a medical condition,
XX PT e.g. Alzheimer's disease, atherosclerosis, myelofibrosis or
XX PT glomerulosclerosis, comprises administering a plasminogen activator
XX PT inhibitor-1 inhibitor.

XX PS Disclosure; Page 59-62; 91pp; English.

XX CC The present sequence is that of cDNA encoding human plasminogen activator
XX CC inhibitor-1 (PAI-1). The PAI-1 gene can be used to produce transgenic
XX CC animals of the invention, useful for screening potential PAI-1
XX CC inhibitors. Such PAI-1 inhibitors can be used to treat a warm-blooded
XX CC vertebrate animal having a medical condition, e.g. alopecia, undesired
XX CC weight loss, Alzheimer's disease, systemic amyloidosis, myelofibrosis,
XX CC glomerulosclerosis, male pattern baldness, keloids, apocrine cysts, acne,
XX CC atherosclerosis, ageing, or a wound (claimed). A method of testing a
XX CC candidate composition for PAI-1 inhibition activity comprises
XX CC administering the composition to a transgenic animal having a PAI-1 gene
XX CC incorporated into its genome, and observing an ameliorating change in the
XX CC animal indicative of inhibition of PAI-1 activity, the change being an
XX CC improvement of a vascular thrombotic disorder, asthma, chronic
XX CC obstructive pulmonary disease, alopecia, undesired weight loss such as
XX CC anorexia, Alzheimer's disease, systemic amyloid deposition, systemic
XX CC amyloidosis, myelofibrosis, glomerulosclerosis, male pattern baldness,
XX CC keloids, apocrine cysts, acne, atherosclerosis, ageing,
XX CC hepatoplenomegaly, extramedullary haematopoiesis, or a wound (claimed)

XX SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 U; 0 Other;

Query Match 100.0%; Score 556; DB 10; Length 2876;
Best Local Similarity 100.0%; Pred. No. 6.5e-137;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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442 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCGGAGC 501
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QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCCGTGACACG 240
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QY 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
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QY 301 CCGGACTCCAGACCCACCGCGGCTCTTCCAAAATCAGACGGCAGCACTGTCTCTGTG 360
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QY 541 AGCCACTGGAAGGCA 556
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Job time : 471.5 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 23:11:40 ; Search time 141.5 Seconds
(without alignments)
6984.624 Million cell updates/sec

Title: US-10-686-428A-4_COPY_238_793

Perfect score: 556

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 9: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	556	100.0	2876	3	US-08-840-204-10
3	556	100.0	2876	3	US-09-324-494A-1
4	556	100.0	2876	3	US-09-324-494A-10
5	556	100.0	2876	3	US-09-023-655-1187
6	114	20.5	1191	3	US-09-016-434-1210
7	114	20.5	2029	9	5187089-1
8	114	20.5	2029	9	5457090-1
9	114	20.5	2029	9	5459001-6
10	114	20.5	2032	9	5187089-3
11	114	20.5	2032	9	5457090-3
12	110.8	19.9	2031	9	5459001-8
13	70.8	12.7	1316	2	US-07-755-461A-12
14	70.6	12.7	1328	2	US-07-679-052A-14
15	70.6	12.7	1340	2	US-07-679-052A-16
16	70.6	12.7	1482	2	US-07-768-286B-5
17	70.6	12.7	1512	2	US-07-768-286B-3
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19	70.6	12.7	1854	3	US-09-023-655-1189
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23	70	12.6	1185	3	US-09-023-339-3
24	70	12.6	1260	3	US-09-023-173-5

25	70	12.6	1308	3	US-09-023-173-10	Sequence 10, Appl
26	70	12.6	1308	3	US-09-023-339-6	Sequence 6, Appl
27	69.2	12.4	1152	2	US-08-315-831A-13	Sequence 13, Appl
28	69.2	12.4	1152	2	US-08-662-318-13	Sequence 13, Appl
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31	69.2	12.4	1316	2	US-08-662-318-12	Sequence 12, Appl
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38	69.2	12.4	1525	3	US-10-014-658-16	Sequence 16, Appl
39	69.2	12.4	1599	3	US-09-328-925-43	Sequence 43, Appl
C 40	69	12.4	241	3	US-09-389-681-338	Sequence 338, App
C 41	69	12.4	241	3	US-09-620-405B-338	Sequence 338, App
C 42	69	12.4	241	3	US-09-433-826B-338	Sequence 338, App
C 43	69	12.4	241	3	US-09-604-287A-338	Sequence 338, App
C 44	69	12.4	241	3	US-09-834-759-338	Sequence 338, App
C 45	69	12.4	241	3	US-09-590-751A-338	Sequence 338, App

ALIGNMENTS

RESULT 1
US-08-840-204-1
; Sequence 1, Application US/08840204
; Patent No. 6103498
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, DANIEL A.
; APPLICANT: STEFANSSON, STEINGRIMUR P.
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
; TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/840,204
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: 30807-20004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 76..1281
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 145
; FEATURE:

NAME/KEY: sig_peptide
LOCATION: 76..144
US-08-840-204-1

Query Match 100.0%; Score 556; DB 3; Length 2876;
Best Local Similarity 100.0%; Pred. No. 2.2e-141; Indels 0; Gaps 0;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 382 AAGGAGCTCATGGGGCCATGGAAACAAAGATGAGATCAGACACAGAGCGCATCTTCGTC 441

QY 61 CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCGGAGC 120
Db 442 CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCGGAGC 501

QY 121 ACGGTCAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTCATCAATCAATCACTGG 180
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QY 421 TACTACGACATCCTGGAATCGCTTACCAACGGGACACCCCTCAGCATGTTCAATTCGCC 480
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Db 862 CTTTATGAAAAGAGTGCTCTCTGCTTACCAACGGGACACCCCTCAGCATGTTCAATTCGCC 921

QY 541 AGCCACTGGAAGGCA 556
Db 922 AGCCACTGGAAGGCA 937

RESULT 2
US-08-840-204-10/c
Sequence 10, Application US/08840204
Patent No. 6103498

GENERAL INFORMATION:
APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSSON, STEINGRIMUR P.
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,204

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30807-20004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030 MESNFOERSWSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-840-204-10

Query Match 100.0%; Score 556; DB 3; Length 2876;
Best Local Similarity 100.0%; Pred. No. 2.2e-141; Indels 0; Gaps 0;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2495 AAGGAGCTCATGGGGCCATGGAAACAAAGATGAGATCAGACACAGAGCGCATCTTCGTC 2436

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QY 541 AGCCACTGGAAGGCA 556
Db 1955 AGCCACTGGAAGGCA 1940

RESULT 3
US-09-324-494A-1
Sequence 1, Application US/09324494A
Patent No. 6489143

GENERAL INFORMATION:
APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSSON, STEINGRIMUR P.
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THEREOF
FILE REFERENCE: 30523/167

; CURRENT APPLICATION NUMBER: US/09/324,494A
; CURRENT FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

; LENGTH: 2876

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (76)..(1281)

; OTHER INFORMATION:

US-09-324-494A-1

Query Match 100.0%; Score 556; DB 3; Length 2876;
Best Local Similarity 100.0%; Pred. No. 2.2e-141;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 382 AAGGAGCTCATGGGCCATGGAACAAGGATGAGATCAGACACACAGCGGATCTTCGTC 441
QY 61 CAGCGGATCTGAAGCTGTCAGAGGCTTCATGCCCACTTCTTCAGGCTGTTCCGAGC 120
DB 442 CAGCGGATCTGAAGCTGTCAGAGGCTTCATGCCCACTTCTTCAGGCTGTTCCGAGC 501
QY 121 ACGGTCAAGCAAGTGACATTTTCAGAGGTGGAGAGCCAGATTCAATCAATGACTGG 180
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QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTCTGGGAAAGAGCCGTTGGACCCAG 240
DB 562 GTGAAGACACACAAAAGGTATGATCAGCAACTTCTGGGAAAGAGCCGTTGGACCCAG 621
QY 241 CTGACACGGCTGCTGTTGATGTCCTTCACTTCAACGGCCAGTGGAGAGCTCCCTTC 300
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QY 301 CCGGACTCAGACACCCACCGCCCTCTTCCAAATCAGACGGGAGCTGTCCTGTG 360
DB 682 CCGGACTCAGACACCCACCGCCCTCTTCCAAATCAGACGGGAGCTGTCCTGTG 741
QY 361 CCATGATGCTCAGACACCAAGTTCACTATCTGAGTTTCACTGAGTTTCACTGAGTTGCCAT 420
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QY 481 CTTATGAAAAGAGTGCTCTCTCTGCCCCTCACCACCAATCTGAGTCCCGAGCTCATC 540
DB 862 CTTATGAAAAGAGTGCTCTCTCTGCCCCTCACCACCAATCTGAGTCCCGAGCTCATC 921
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DB 922 AGCCACTGGAAGGCA 937

RESULT 4

US-09-324-494A-10/c

; Sequence 10, Application US/09324494A

; Patent No. 6489143

; GENERAL INFORMATION:

; APPLICANT: LAWRENCE, Daniel A

; APPLICANT: STEFANSON, Steingrur P

; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES TH

; FILE REFERENCE: 30523/167

; CURRENT APPLICATION NUMBER: US/09/324,494A

; CURRENT FILING DATE: 1999-06-02

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 2876

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-324-494A-10

Query Match 100.0%; Score 556; DB 3; Length 2876;

Best Local Similarity 100.0%; Pred. No. 2.2e-141;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCCATGGAACAAGGATGAGATCAGACACACAGCGGATCTTCGTC 60
DB 2495 AAGGAGCTCATGGGCCATGGAACAAGGATGAGATCAGACACACAGCGGATCTTCGTC 2436
QY 61 CAGCGGATCTGAAGCTGTCAGAGGCTTCATGCCCACTTCTTCAGGCTGTTCCGAGC 120
DB 2435 CAGCGGATCTGAAGCTGTCAGAGGCTTCATGCCCACTTCTTCAGGCTGTTCCGAGC 2376
QY 121 ACGGTCAAGCAAGTGACATTTTCAGAGGTGGAGAGCCAGATTCAATCAATGACTGG 180
DB 2375 ACGGTCAAGCAAGTGACATTTTCAGAGGTGGAGAGCCAGATTCAATCAATGACTGG 2316
QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTCTGGGAAAGAGCCGTTGGACCCAG 240
DB 2315 GTGAAGACACACAAAAGGTATGATCAGCAACTTCTGGGAAAGAGCCGTTGGACCCAG 2256
QY 241 CTGACACGGCTGCTGTTGATGTCCTTCACTTCAACGGCCAGTGGAGAGCTCCCTTC 300
DB 2255 CTGACACGGCTGCTGTTGATGTCCTTCACTTCAACGGCCAGTGGAGAGCTCCCTTC 2196
QY 301 CCGGACTCAGACACCCACCGCCCTCTTCCAAATCAGACGGGAGCTGTCCTGTG 360
DB 2195 CCGGACTCAGACACCCACCGCCCTCTTCCAAATCAGACGGGAGCTGTCCTGTG 2136
QY 361 CCATGATGCTCAGACACCAAGTTCACTATCTGAGTTTCACTGAGTTTCACTGAGTTGCCAT 420
DB 2135 CCATGATGCTCAGACACCAAGTTCACTATCTGAGTTTCACTGAGTTTCACTGAGTTGCCAT 2076
QY 421 TACTACGACATCTGGAACCTGACCGGGACACCTCAGCATGTTTCACTGAGTTGTCGCC 480
DB 2075 TACTACGACATCTGGAACCTGACCGGGACACCTCAGCATGTTTCACTGAGTTGTCGCC 2016
QY 481 CTTATGAAAAGAGTGCTCTCTCTGCCCCTCACCACCAATCTGAGTCCCGAGCTCATC 540
DB 2015 CTTATGAAAAGAGTGCTCTCTCTGCCCCTCACCACCAATCTGAGTCCCGAGCTCATC 1956
QY 541 AGCCACTGGAAGGCA 556
DB 1955 AGCCACTGGAAGGCA 1940

RESULT 5

US-09-023-655-1187

; Sequence 1187, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESS: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,294
; FILING DATE: 03-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 542,484
; FILING DATE: 21-JUN-1990
;

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Qy 230 CCGTGGG---CCAGCTGACACCGGCTGGTGTGAATGCCCTCTACTTTCAACGGCCAGT 286
Db 662 TTATTGATGGTGTCTCACCAGACTGGTCTCTGCTCAACGAGTGTATTTCAGGGTCTGT 721
Qy 287 GGAAGACTCCCTTCCCGAGCTCCAGACCCACCGCGGCTCTTCCACAAATCAGACGGCA 346
Db 722 GGAATACACGGTTTCAACCGGAGAACACAAAGAAACGCACTTTCGTGGCAGCGGAGGA 781
Qy 347 GCACCTGTCTCTGTGCGCATGATGGCTCAGACCAACAAAGTTCACTATCTAGTTTACCA 406
Db 782 AATCCTATCAAGTGCCAAATGCTGGCCAGCTCTCCGCTGTTCGGTGTGGTGCACAAAGTG 841
Qy 407 CGCCCGATGGCCATTACTACGACATCTCTGGAACTCCCTTACCACGGGACACCCCTCAGCA 466
Db 842 CCCCCAATGATTATGATGATCAACTTCAATGAATGCCCTTACCACGGGAAAGCATCAGCA 901
Qy 467 TGTTCATTGTGCTCCCTTTATGAAAAGAGGTGCTCTCTCTGCCCTCACCACAACTTCTGA 526
Db 902 TGCTGATTGCACTGCGGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATCA 961
Qy 527 GTGCCAGCTCATAGCCACTCGGAAGGCA 556
Db 962 GCACCAAGACCATAGACAGCTGGATGAGCA 991

RESULT 10
5187089-3
; Patent No. 5187089
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS WHICH INHIBIT ELASTASE
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO: 3
; LENGTH: 2032
5187089-3

Query Match 20.5%; Score 114; DB 9; Length 2032;
Best Local Similarity 54.9%; Pred. No. 4e-21;
Matches 247; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

Qy 110 TGTTCGGAGCAGCTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTCATCA 169
Db 542 TGTTCAGTGTGAGTCCGGAATGTGAATTTGAGGATCCAGCCTCTGCTGTGATTCCA 601
Qy 170 TCAATGACTGGGTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGGAG 229
Db 602 TCAATGATGGTTHAAACGAAACGAGGATATGATTGACAATCTGCTGTCCCGAGATC 661
Qy 230 CCGTGGG---CCAGCTGACACCGGCTGGTGTGAATGCCCTCTACTTTCAACGGCCAGT 286
Db 662 TTATTGATGGTGTCTCACCAGACTGGTCTCTGCTCAACGAGTGTATTTCAGGGTCTGT 721
Qy 287 GGAAGACTCCCTTCCCGAGCTCAGACCCACCGCGGCTCTTCCACAAATCAGACGGCA 346
Db 722 GGAATACACGGTTTCAACCGGAGAACACAAAGAAACGCACTTTCGTGGCAGCGGAGGA 781
Qy 347 GCACCTGTCTGTGCGCATGATGGCTCAGACCAACAAAGTTCACTATCTAGTTTACCA 406
Db 782 AATCCTATCAAGTGCCAAATGCTGGCCAGCTCTCCGCTGTTCGGTGTGGTGCACAAAGTG 841
Qy 407 CGCCCGATGGCCATTACTACGACATCTCTGGAACTCCCTTACCACGGGACACCCCTCAGCA 466
Db 842 CCCCCAATGATTATGATGATCAACTTCAATGAATGCCCTTACCACGGGAAAGCATCAGCA 901
Qy 467 TGTTCATTGTGCTCCCTTTATGAAAAGAGGTGCTCTCTCTGCCCTCACCACAACTTCTGA 526
Db 902 TGCTGATTGCACTGCGGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATCA 961

Qy 527 GTGCCAGCTCATCAGCCACTCGGAAGGCA 556
Db 962 GCACCAAGACCATAGACAGCTGGATGAGCA 991

RESULT 11
5457090-3
; Patent No. 5457090
; APPLICANT: SCOTT, RANDY W.; GOLINI, FRED; MCGROGAN, MICHAEL
; TITLE OF INVENTION: PROTEASE NEXIN-I VARIANTS
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/924,294
; FILING DATE: 03-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 542,484
; FILING DATE: 21-JUN-1990
; SEQ ID NO: 3
; LENGTH: 2032
5457090-3

Query Match 20.5%; Score 114; DB 9; Length 2032;
Best Local Similarity 54.9%; Pred. No. 4e-21;
Matches 247; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

Qy 110 TGTTCGGAGCAGCTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTCATCA 169
Db 542 TGTTCAGTGTGAGTCCGGAATGTGAATTTGAGGATCCAGCCTCTGCTGTGATTCCA 601
Qy 170 TCAATGACTGGGTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGGAG 229
Db 602 TCAATGATGGTTHAAACGAAACGAGGATATGATTGACAATCTGCTGTCCCGAGATC 661
Qy 230 CCGTGGG---CCAGCTGACACCGGCTGGTGTGAATGCCCTCTACTTTCAACGGCCAGT 286
Db 662 TTATTGATGGTGTCTCACCAGACTGGTCTCTGCTCAACGAGTGTATTTCAGGGTCTGT 721
Qy 287 GGAAGACTCCCTTCCCGAGCTCAGACCCACCGCGCTCTTCCACAAATCAGACGGCA 346
Db 722 GGAATACACGGTTTCAACCGGAGAACACAAAGAAACGCACTTTCGTGGCAGCGGAGGA 781
Qy 347 GCACCTGTCTGTGCGCATGATGGCTCAGACCAACAAAGTTCACTATCTAGTTTACCA 406
Db 782 AATCCTATCAAGTGCCAAATGCTGGCCAGCTCTCGGTGTCGGTGTGGTGCACAAAGTG 841
Qy 407 CGCCCGATGGCCATTACTACGACATCTCTGGAACTCCCTTACCACGGGACACCCCTCAGCA 466
Db 842 CCCCCAATGATTATGATGATCAACTTCAATGAATGCCCTTACCACGGGAAAGCATCAGCA 901
Qy 467 TGTTCATTGTGCTCCCTTTATGAAAAGAGGTGCTCTCTCTGCCCTCACCACAACTTCTGA 526
Db 902 TGCTGATTGCACTGCGGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATCA 961
Qy 527 GTGCCAGCTCATCAGCCACTCGGAAGGCA 556
Db 962 GCACCAAGACCATAGACAGCTGGATGAGCA 991

RESULT 12
5495001-8
; Patent No. 5495001
; APPLICANT: MCGROGAN, MICHAEL P.; SCOTT, RANDY W.; BAKER,
; JOFFRE B.; SIMONSEN, CHRISTIAN C.
; TITLE OF INVENTION: RECOMBINANT PURIFIED PROTEASE NEXIN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,596
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 111,111
; FILING DATE: 24-AUG-1993
; APPLICATION NUMBER: 25,450

```

RESULT 14
US-07-679-052A-14
; Sequence 14, Application US/07679052A
; Patent No. 5298400
; GENERAL INFORMATION:
; APPLICANT: WHITFELD, Peter L.
; APPLICANT: RICHARDSON, Michael A.
; APPLICANT: BUNN, Clive L.
; TITLE OF INVENTION: RECOMBINANT PRODUCT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Vers
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,052A
; FILING DATE: 19910506

```

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/147 CHAC
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
FEATURE:
NAME/KEY: CDS
LOCATION: 15..1319
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 15..71
OTHER INFORMATION: /product= "Synthetic signal"
OTHER INFORMATION: peptide"
US-07-679-052A-14

Query Match 12.7%; Score 70.6; DB 2; Length 1328;
Best Local Similarity 67.1%; Pred. No. 2.2e-09;
Matches 100; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
Qy 151 GAGAGAGCCAGATTCATCATCAATGACTGGGTGAAGACACACACAAAAGGTATGATCAGC 210
Db 558 GAAGAGCTAGAAAAAGATTAAATTCCTGGGTCAAGACTCAAAACCAAGGCAAAATCCCA 617
Qy 211 AACTTGTCTGGGAAGAGCGCTGGACACAGCTGACACGGCTGGTCTGGTGAATGCCCTC 270
Db 618 AACTTGTACCTGAAGGTTCTGTAGATGGGATACCAGATGGTCTGTGAATGCTGTC 677
Qy 271 TACTTCAAGCGCCAGTGAAGACTCCCTT 299
Db 678 TACTTCAAGGAAGTGGAAAACTCCATT 706

RESULT 15
US-07-679-052A-16
Sequence 16, Application US/07679052A
Patent No. 5298400
GENERAL INFORMATION:
APPLICANT: WHITEFELD, Peter L.
APPLICANT: RICHARDSON, Michael A.
APPLICANT: BUNN, Clive L.
TITLE OF INVENTION: RECOMBINANT PRODUCT
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679,052A
FILING DATE: 19910506
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16786/147 CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1340 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
FEATURE:
NAME/KEY: CDS
LOCATION: 15..1331
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 15..86
OTHER INFORMATION: /product= "a-1-antitrypsin signal"
US-07-679-052A-16

Query Match 12.7%; Score 70.6; DB 2; Length 1340;
Best Local Similarity 67.1%; Pred. No. 2.2e-09;
Matches 100; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
Qy 151 GAGAGAGCCAGATTCATCATCAATGACTGGGTGAAGACACACACAAAAGGTATGATCAGC 210
Db 570 GAAGAGCTAGAAAAAGATTAAATTCCTGGGTCAAGACTCAAAACCAAGGCAAAATCCCA 629
Qy 211 AACTTGTCTGGGAAGAGCGCTGGACACAGCTGACACGGCTGGTCTGGTGAATGCCCTC 270
Db 630 AACTTGTACCTGAAGGTTCTGTAGATGGGATACCAGATGGTCTGTGAATGCTGTC 689
Qy 271 TACTTCAAGCGCCAGTGAAGACTCCCTT 299
Db 690 TACTTCAAGGAAGTGGAAAACTCCATT 718

Search completed: March 10, 2006, 01:05:59
Job time : 141.5 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	556	100.0	1209	6	US-10-128-706-17	Sequence 17, Appl
2	556	100.0	1209	9	US-10-512-496-17	Sequence 17, Appl
3	556	100.0	1962	6	US-10-368-995-5	Sequence 5, Appl
4	556	100.0	2177	9	US-10-852-335A-45	Sequence 45, Appl
5	556	100.0	2660	3	US-09-814-353-20146	Sequence 20146, A
6	556	100.0	2870	5	US-10-060-036-131	Sequence 131, App
7	556	100.0	2876	6	US-10-128-706-5	Sequence 5, Appl
8	556	100.0	2876	6	US-10-170-385-236	Sequence 236, App
9	556	100.0	2876	6	US-10-259-609-1	Sequence 1, Appl
10	556	100.0	2876	6	US-10-259-609-10	Sequence 10, Appl
11	556	100.0	2876	6	US-10-368-995-3	Sequence 3, Appl
12	556	100.0	2876	7	US-10-191-258-1	Sequence 1, Appl
13	556	100.0	2876	7	US-10-231-956A-419	Sequence 419, App
14	556	100.0	2876	7	US-10-641-643-1187	Sequence 1187, Ap
15	556	100.0	2876	9	US-10-956-157-442	Sequence 442, App
16	556	100.0	2876	9	US-10-512-496-5	Sequence 5, Appl
17	556	100.0	2876	9	US-10-506-406-1	Sequence 1, Appl
18	556	100.0	2876	9	US-10-631-467-399	Sequence 399, App
19	556	100.0	2937	8	US-10-775-169-229	Sequence 229, App
20	556	100.0	3171	6	US-10-240-965-160	Sequence 160, App
21	556	100.0	3172	5	US-10-044-090-842	Sequence 842, App
22	556	100.0	3172	5	US-10-084-817-6	Sequence 6, Appl
23	554.4	99.7	1482	5	US-10-193-656-9	Sequence 9, Appl

QY 361 CCCATGATGGCTCAGACCAACAGATTCAACTATCTAGATTACACACGCCGATGGCCAT 420
Db 667 CCCATGATGGCTCAGACCAACAGATTCAACTATCTAGATTACACACGCCGATGGCCAT 726
QY 421 TACTACGACATCCTGGAACTGCGCTTACCACGGGGACACCTCAGCATGTTCAATCTGCTGCC 480
Db 727 TACTACGACATCCTGGAACTGCGCTTACCACGGGGACACCTCAGCATGTTCAATCTGCTGCC 786
QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCGCTTACCACAACTTCTGAGTGCCAGCTCATC 540
Db 787 CTTTATGAAAAGAGTGCTCTCTCTGCGCTTACCACAACTTCTGAGTGCCAGCTCATC 846
QY 541 AGCCACTGGAAGGCA 556
Db 847 AGCCACTGGAAGGCA 862

RESULT 2
US-10-512-496-17
; Sequence 17, Application US/10512496
; Publication No. US20050148527A1
; GENERAL INFORMATION:
; APPLICANT: ITESCU, SILVIU
; TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1
; FILE REFERENCE: 0575/66601-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/512,496
; CURRENT FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-512-496-17

Query Match 100.0%; Score 556; DB 9; Length 1209;
Best Local Similarity 100.0%; Pred. No. 3.5e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCCATGGAAACAGATGATCAGCACACAGACCGCATCTTCGTC 60
Db 307 AAGGAGCTCATGGGCGCCATGGAAACAGATGATCAGCACACAGACCGCATCTTCGTC 366
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCGCTTCTTCAGGCTGTTCGGGAGC 120
Db 367 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCGCTTCTTCAGGCTGTTCGGGAGC 426
QY 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCGCAGATTCAATCAATGACTGG 180
Db 427 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCGCAGATTCAATCAATGACTGG 486
QY 181 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGGAAAGGAGCGGTGGACGAG 240
Db 487 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGGAAAGGAGCGGTGGACGAG 546
QY 241 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCGAGTGGAAAGACTCCCTTC 300
Db 547 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCGAGTGGAAAGACTCCCTTC 606
QY 301 CCCGACTCCAGCACCGACCGCGCTTTCACAAATCAGACGGCAGCACTGTCTCTGTG 360
Db 607 CCCGACTCCAGCACCGACCGCGCTTTCACAAATCAGACGGCAGCACTGTCTCTGTG 666
QY 361 CCCATGATGGCTCAGACCAACAGTTCAACTATCTAGATTACACACGCCGATGGCCAT 420
Db 667 CCCATGATGGCTCAGACCAACAGTTCAACTATCTAGATTACACACGCCGATGGCCAT 726
QY 421 TACTACGACATCCTGGAACTGCGCTTACCACGGGGACACCTCAGCATGTTCAATCTGCTGCC 480
Db 727 TACTACGACATCCTGGAACTGCGCTTACCACGGGGACACCTCAGCATGTTCAATCTGCTGCC 786
QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCGCTTACCACAACTTCTGAGTGCCAGCTCATC 540

Db 787 CTTTATGAAAAGAGTGCTCTCTCTGCGCTTACCACAACTTCTGAGTGCCAGCTCATC 846
QY 541 AGCCACTGGAAGGCA 556
Db 847 AGCCACTGGAAGGCA 862

RESULT 3
US-10-368-995-5
; Sequence 5, Application US/10368995
; Publication No. US20030217371A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Douglas E.
; APPLICANT: Eren, Mesut
; APPLICANT: Declerk, Paul J.
; TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON-
; FILE REFERENCE: 1242/43
; CURRENT APPLICATION NUMBER: US/10/368,995
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1962
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1161)
; OTHER INFORMATION:
US-10-368-995-5

Query Match 100.0%; Score 556; DB 6; Length 1962;
Best Local Similarity 100.0%; Pred. No. 4.1e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCCATGGAAACAGATGATCAGCACACAGACCGCATCTTCGTC 60
Db 259 AAGGAGCTCATGGGCGCCATGGAAACAGATGATCAGCACACAGACCGCATCTTCGTC 318
QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCGCTTCTTCAGGCTGTTCGGGAGC 120
Db 319 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCGCTTCTTCAGGCTGTTCGGGAGC 378
QY 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCGCAGATTCAATCAATGACTGG 180
Db 379 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCGCAGATTCAATCAATGACTGG 438
QY 181 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGGAAAGGAGCGGTGGACGAG 240
Db 439 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGGAAAGGAGCGGTGGACGAG 498
QY 241 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCGAGTGGAAAGACTCCCTTC 300
Db 499 CTGACACGGCTGGTGTGTAATGCCCTCTACTTCAACGGCGAGTGGAAAGACTCCCTTC 558
QY 301 CCCGACTCCAGCACCGACCGCGCTTTCACAAATCAGACGGCAGCACTGTCTCTGTG 360
Db 559 CCCGACTCCAGCACCGACCGCGCTTTCACAAATCAGACGGCAGCACTGTCTCTGTG 618
QY 361 CCCATGATGGCTCAGACCAACAGTTCAACTATCTAGATTACACACGCCGATGGCCAT 420
Db 619 CCCATGATGGCTCAGACCAACAGTTCAACTATCTAGATTACACACGCCGATGGCCAT 678
QY 421 TACTACGACATCCTGGAACTGCGCTTACCACGGGGACACCTCAGCATGTTCAATCTGCTGCC 480
Db 679 TACTACGACATCCTGGAACTGCGCTTACCACGGGGACACCTCAGCATGTTCAATCTGCTGCC 738
QY 481 CTTTATGAAAAGAGTGCTCTCTCTGCGCTTACCACAACTTCTGAGTGCCAGCTCATC 540
Db 739 CTTTATGAAAAGAGTGCTCTCTCTGCGCTTACCACAACTTCTGAGTGCCAGCTCATC 798
QY 541 AGCCACTGGAAGGCA 556

Db 799 AGCCACTGGAAAGGCA 814
|||||

RESULT 4

US-10-852-335A-45

; Sequence 45, Application US/10852335A

; Publication No. US20050112129A1

; GENERAL INFORMATION:

; APPLICANT: HEIDI S. PHILLIPS

; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and Treatment of Tumors of Glial Origin

; FILE REFERENCE: P5103R1-US

; CURRENT APPLICATION NUMBER: US/10/852,335A

; CURRENT FILING DATE: 2004-05-24

; PRIOR APPLICATION NUMBER: US 60/548,299

; PRIOR FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US 60/473,238

; PRIOR FILING DATE: 2003-05-23

; NUMBER OF SEQ ID NOS: 190

; SEQ ID NO 45

; LENGTH: 2177

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-852-335A-45

Query Match 100.0%; Score 556; DB 9; Length 2177;

Best Local Similarity 100.0%; Pred. No. 4.3e-166;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAGGAGCTCATGGGCCATGGAACAAGGATGAGATCAGACACACAGCGGATCTTCGTC	60
Db	414	AAGGAGCTCATGGGCCATGGAACAAGGATGAGATCAGACACACAGCGGATCTTCGTC	473
QY	61	CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCACCTCTTTCAGGCTGTTCGGAGC	120
Db	474	CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCACCTCTTTCAGGCTGTTCGGAGC	533
QY	121	ACGGTCAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG	180
Db	534	ACGGTCAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG	593
QY	181	GTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGTTGGACCG	240
Db	594	GTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGTTGGACCG	653
QY	241	CTGACACGGCTGTGTGTGTAATGCGCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC	300
Db	654	CTGACACGGCTGTGTGTGTAATGCGCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC	713
QY	301	CCGACTCCAGACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG	360
Db	714	CCGACTCCAGACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG	773
QY	361	CCCATGATGCTCAGACCAAGTTCACATATCTAGTGTACACGCGCCGATGCCAT	420
Db	774	CCCATGATGCTCAGACCAAGTTCACATATCTAGTGTACACGCGCCGATGCCAT	833
QY	421	TACTAGACATCTGGAAGTCCCTACCGGGGACACCTCAGCATGTTTCATTTGTG	480
Db	834	TACTAGACATCTGGAAGTCCCTACCGGGGACACCTCAGCATGTTTCATTTGTG	893
QY	481	CCTTATGAAAAGAGTGTCTCTCTGCGCTCACCACAAATCTGAGTGCCAGCTCATC	540
Db	894	CCTTATGAAAAGAGTGTCTCTCTGCGCTCACCACAAATCTGAGTGCCAGCTCATC	953
QY	541	AGCCACTGGAAAGGCA 556	
Db	954	AGCCACTGGAAAGGCA 969	

RESULT 5

US-09-814-353-20146

; Sequence 20146, Application US/09814353
; Publication No. US20030165831A1

; GENERAL INFORMATION:

; APPLICANT: Thompson, Pamela

; APPLICANT: Lillie, James

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF OVARIAN CANCER

; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

; FILE REFERENCE: MRI-006B

; CURRENT APPLICATION NUMBER: US/09/814,353

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/191,031

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/207,124

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: US 60/211,940

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: US 60/216,820

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/220,661

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: US 60/257,672

; PRIOR FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 22037

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20146

; LENGTH: 2660

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-814-353-20146

Query Match 100.0%; Score 556; DB 3; Length 2660;

Best Local Similarity 100.0%; Pred. No. 4.6e-166;

Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAGGAGCTCATGGGCCATGGAACAAGGATGAGATCAGACACACAGCGGATCTTCGTC	60
Db	452	AAGGAGCTCATGGGCCATGGAACAAGGATGAGATCAGACACACAGCGGATCTTCGTC	511
QY	61	CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCACCTCTTTCAGGCTGTTCGGAGC	120
Db	512	CAGCGGATCTGAAGCTGTGTCAGGGCTTCATGCCACCTCTTTCAGGCTGTTCGGAGC	571
QY	121	ACGGTCAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG	180
Db	572	ACGGTCAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG	631
QY	181	GTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGTTGGACCG	240
Db	632	GTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGTTGGACCG	691
QY	241	CTGACACGGCTGTGTGTGTAATGCGCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC	300
Db	692	CTGACACGGCTGTGTGTGTAATGCGCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC	751
QY	301	CCGACTCCAGACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG	360
Db	752	CCGACTCCAGACCCACCGCGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG	811
QY	361	CCCATGATGCTCAGACCAAGTTCACATATCTAGTGTACCAACCGCCGATGCCAT	420
Db	812	CCCATGATGCTCAGACCAAGTTCACATATCTAGTGTACCAACCGCCGATGCCAT	871
QY	421	TACTAGACATCTGGAAGTCCCTACCGGGGACACCTCAGCATGTTTCATTTGTG	480
Db	872	TACTAGACATCTGGAAGTCCCTACCGGGGACACCTCAGCATGTTTCATTTGTG	931
QY	481	CCTTATGAAAAGAGTGTCTCTCTGCGCTCACCACAAATCTGAGTGCCAGCTCATC	540
Db	932	CCTTATGAAAAGAGTGTCTCTCTGCGCTCACCACAAATCTGAGTGCCAGCTCATC	991
QY	541	AGCCACTGGAAAGGCA 556	

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DB      992 AGCCACTGGAAGGCA 1007
|||||
RESULT 6
US-10-060-036-131
; Sequence 131, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 2870
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-131

Query Match      100.0%; Score 556; DB 5; Length 2870;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAGGAGCTCATGGGCGCATGGAACAAAGGATGAGATCAGCACACAGCGCGATCTTCGTC 60
DB      376 AAGGAGCTCATGGGCGCATGGAACAAAGGATGAGATCAGCACACAGCGCGATCTTCGTC 435
QY      61 CAGCGGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 120
DB      436 CAGCGGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 495
QY      121 AGGTCAGCAAGTGACATTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 180
DB      496 AGGTCAGCAAGTGACATTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 555
QY      181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
DB      556 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 615
QY      241 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGGGAAGACTCCCTTC 300
DB      616 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGGGAAGACTCCCTTC 675
QY      301 CCGGACTCAGACACCCACCGCGCTCTTCCACAAATCAGACGGAGCACTGTCTCTGTG 360
DB      676 CCGGACTCAGACACCCACCGCGCTCTTCCACAAATCAGACGGAGCACTGTCTCTGTG 735
QY      361 CCCATGATGGCTCAGACCAACAGTTCAACTACTGTAGTTCAACACCCCGATGCCAT 420
DB      736 CCCATGATGGCTCAGACCAACAGTTCAACTACTGTAGTTCAACACCCCGATGCCAT 795
QY      421 TACTACGACATCTGGAACTGCCCTACACGGGGACACCCCTCAGCATGTTCAATGCTGCC 480
DB      796 TACTACGACATCTGGAACTGCCCTACACGGGGACACCCCTCAGCATGTTCAATGCTGCC 855
QY      481 CTTTATGAAAAAGAGTGCTCTCTCTGCGCTTCAACAAATTTCTGAGTGCCCGAGTCTATC 540
DB      856 CTTTATGAAAAAGAGTGCTCTCTCTGCGCTTCAACAAATTTCTGAGTGCCCGAGTCTATC 915
QY      541 AGCCACTGGAAGGCA 556
DB      916 AGCCACTGGAAGGCA 931

RESULT 7
US-10-128-706-5
; Sequence 5, Application US/10128706
; Publication No. US20030199463A1
; GENERAL INFORMATION:
; APPLICANT: ITESCU, SILVIU
; FILE REFERENCE: 0575/66601
; CURRENT APPLICATION NUMBER: US/10/128,706
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-128-706-5

Query Match      100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAGGAGCTCATGGGCGCATGGAACAAAGGATGAGATCAGCACACAGCGCGATCTTCGTC 60
DB      382 AAGGAGCTCATGGGCGCATGGAACAAAGGATGAGATCAGCACACAGCGCGATCTTCGTC 441
QY      61 CAGCGGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 120
DB      442 CAGCGGGATCTGAAGCTGGTCCAGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC 501
QY      121 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 180
DB      502 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 561
QY      181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
DB      562 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 621
QY      241 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGGGAAGACTCCCTTC 300
DB      622 CTGACACGGCTGGTGGTGAATGCCCTTACTTCAACGGCCAGTGGGAAGACTCCCTTC 681
QY      301 CCGGACTCAGACACCCACCGCGCTCTTCCACAAATCAGACGGGAGCACTGTCTCTGTG 360
DB      682 CCGGACTCAGACACCCACCGCGCTCTTCCACAAATCAGACGGGAGCACTGTCTCTGTG 741
QY      361 CCCATGATGGCTCAGACCAACAAAGTTCAATATCTAGTTTCAACACCGCCGATGCCAT 420
DB      742 CCCATGATGGCTCAGACCAACAAAGTTCAATATCTAGTTTCAACACCGCCGATGCCAT 801
QY      421 TACTACGACATCTGGAACTGCCCTACACGGGGACACCCCTCAGCATGTTCAATGCTGCC 480
DB      802 TACTACGACATCTGGAACTGCCCTACACGGGGACACCCCTCAGCATGTTCAATGCTGCC 861
QY      481 CTTTATGAAAAAGAGTGCTCTCTCTGCGCTTCAACAAATTTCTGAGTGCCCGAGTCTATC 540
DB      862 CTTTATGAAAAAGAGTGCTCTCTCTGCGCTTCAACAAATTTCTGAGTGCCCGAGTCTATC 921
QY      541 AGCCACTGGAAGGCA 556
DB      922 AGCCACTGGAAGGCA 937

RESULT 8
US-10-170-385-236
; Sequence 236, Application US/10170385
; Publication No. US2003020372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
```


APPLICANT: Binley, Katie Mary
APPLICANT: Rayner, William Nigel
APPLICANT: Naylor, Stuart
APPLICANT: Kingsman, Susan Mary
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 53268200100
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-05-12
PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 236
LENGTH: 2876
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-170-385-236

Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCATGGAACAAGGATGAGATCAGACCCAGACGCGATCTTCGTC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
382 AAGGAGCTCATGGGCGCATGGAACAAGGATGAGATCAGACCCAGACGCGATCTTCGTC 441
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCCCGAGC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
442 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCCCGAGC 501
QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
502 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 561
QY 181 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGGAAAGAGCGCGTGACCG 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
562 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGGAAAGAGCGCGTGACCG 621
QY 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
622 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 681
QY 301 CCGGACTCCAGACCCACCGCGCTCTTCCAAATTCAGACGGCAGCACTGTCTGTG 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
682 CCGGACTCCAGACCCACCGCGCTCTTCCAAATTCAGACGGCAGCACTGTCTGTG 741
QY 361 CCCATGATGCTCAGACCAAGTTCACTATCTAGTTCACCGCCGCGATGGCCAT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
742 CCCATGATGCTCAGACCAAGTTCACTATCTAGTTCACCGCCGCGATGGCCAT 801
QY 421 TACTAGACATCTGGAACTGCCCTACCGGGGACACCTCAGCATGTTTCATTGTGCC 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
802 TACTAGACATCTGGAACTGCCCTACCGGGGACACCTCAGCATGTTTCATTGTGCC 861
QY 481 CTTATGAAAAGAGTGCTCTCTGCGCCCTCACCACAAATTCAGTGCGCCAGCTCATC 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
862 CTTATGAAAAGAGTGCTCTCTGCGCCCTCACCACAAATTCAGTGCGCCAGCTCATC 921
QY 541 AGCCACTGGAAAGGCA 556
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
922 AGCCACTGGAAAGGCA 937

RESULT 9
US-10-259-609-1
Sequence 1, Application US/10259609
Publication No. US20030216321A1
GENERAL INFORMATION:
APPLICANT: LAWRENCE, Daniel A
APPLICANT: STEFANSSON, Steingrur P

TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THE
FILE REFERENCE: 30523/167
CURRENT APPLICATION NUMBER: US/10/259,609
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US/09/324,494A
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2876
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (76)..(1281)
OTHER INFORMATION:
US-10-259-609-1

Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCATGGAACAAGGATGAGATCAGACCCAGACGCGATCTTCGTC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
382 AAGGAGCTCATGGGCGCATGGAACAAGGATGAGATCAGACCCAGACGCGATCTTCGTC 441
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCCCGAGC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
442 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTTCAGGCTGTTCCCGAGC 501
QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
502 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCAATGACTGG 561
QY 181 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGGAAAGAGCGCGTGACCG 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
562 GTGAAGACACACAAAGGTATGATCAGCAACTTGTCTGGGAAAGAGCGCGTGACCG 621
QY 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
622 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 681
QY 301 CCGGACTCCAGACCCACCGCGCTCTTCCAAATTCAGACGGCAGCACTGTCTGTG 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
682 CCGGACTCCAGACCCACCGCGCTCTTCCAAATTCAGACGGCAGCACTGTCTGTG 741
QY 361 CCCATGATGCTCAGACCAAGTTCACTATCTAGTTCACCGCCGCGATGGCCAT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
742 CCCATGATGCTCAGACCAAGTTCACTATCTAGTTCACCGCCGCGATGGCCAT 801
QY 421 TACTAGACATCTGGAACTGCCCTACCGGGGACACCTCAGCATGTTTCATTGTGCC 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
802 TACTAGACATCTGGAACTGCCCTACCGGGGACACCTCAGCATGTTTCATTGTGCC 861
QY 481 CTTATGAAAAGAGTGCTCTCTGCGCCCTCACCACAAATTCAGTGCGCCAGCTCATC 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
862 CTTATGAAAAGAGTGCTCTCTGCGCCCTCACCACAAATTCAGTGCGCCAGCTCATC 921
QY 541 AGCCACTGGAAAGGCA 556
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
922 AGCCACTGGAAAGGCA 937

RESULT 10
US-10-259-609-10/c
Sequence 10, Application US/10259609
Publication No. US20030216321A1
GENERAL INFORMATION:
APPLICANT: LAWRENCE, Daniel A
APPLICANT: STEFANSSON, Steingrur P
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THE
FILE REFERENCE: 30523/167
CURRENT APPLICATION NUMBER: US/10/259,609

; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/324,494A
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-259-609-10

Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCATCGAACAGGATGATCAGCACACAGCGCGATCTTCGTC 60
DB 2495 AAGGAGCTCATGGGCGCATCGAACAGGATGATCAGCACACAGCGCGATCTTCGTC 2436
QY 61 CAGCGGGATCTGAAGCTGCTCCAGGGCTTCATGCCCCACTTCTTCAGGGTGTTCGGAGC 120
DB 2435 CAGCGGGATCTGAAGCTGCTCCAGGGCTTCATGCCCCACTTCTTCAGGGTGTTCGGAGC 2376
QY 121 AGGTCACAGCAAGTGACCTTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 180
DB 2375 AGGTCACAGCAAGTGACCTTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 2316
QY 181 GTGAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
DB 2315 GTGAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 2256
QY 241 CTGACACGGCTGTGCTGGTGAATGCTCTACTTCAACGGCCAGTGAAGACTCCCTTC 300
DB 2255 CTGACACGGCTGTGCTGGTGAATGCTCTACTTCAACGGCCAGTGAAGACTCCCTTC 2196
QY 301 CCGGACTCCAGCACCCACCGCGCCCTCTTCCAAATCAGACGGCAGCACTGTCTGTG 360
DB 2195 CCGGACTCCAGCACCCACCGCGCCCTCTTCCAAATCAGACGGCAGCACTGTCTGTG 2136
QY 361 CCCATGATGGCTCAGACCAACAGTTCAACTATCTAGTTTCCACCGCCGATGGCCAT 420
DB 2135 CCCATGATGGCTCAGACCAACAGTTCAACTATCTAGTTTCCACCGCCGATGGCCAT 2076
QY 421 TACTACGACATCTGGAACTGGCCCTACACGGGGACACCCCTCAGCATGTTCAATTGCTGC 480
DB 2075 TACTACGACATCTGGAACTGGCCCTACACGGGGACACCCCTCAGCATGTTCAATTGCTGC 2016
QY 481 CTTTATGAAAAAGAGTGCTCTCTGCTCCCTCACCAACATTCTGAGTGCCCGAGCTCATC 540
DB 2015 CTTTATGAAAAAGAGTGCTCTCTGCTCCCTCACCAACATTCTGAGTGCCCGAGCTCATC 1956
QY 541 AGCCACTGGAAGGCA 556
DB 1955 AGCCACTGGAAGGCA 1940

RESULT 11
US-10-368-995-3
; Sequence 3, Application US/10368995
; Publication No. US20030217371A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Douglas E.
; APPLICANT: Eren, Mesut
; APPLICANT: Declerk, Paul J.
; TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON
; FILE REFERENCE: 1242/43
; CURRENT APPLICATION NUMBER: US/10/368,995
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2876

; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1284)
; OTHER INFORMATION:
US-10-368-995-3

Query Match 100.0%; Score 556; DB 6; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGCGCATCGAACAGGATGATCAGCACACAGCGCGATCTTCGTC 60
DB 382 AAGGAGCTCATGGGCGCATCGAACAGGATGATCAGCACACAGCGCGATCTTCGTC 441
QY 61 CAGCGGGATCTGAAGCTGCTCCAGGGCTTCATGCCCCACTTCTTCAGGGTGTTCGGAGC 120
DB 442 CAGCGGGATCTGAAGCTGCTCCAGGGCTTCATGCCCCACTTCTTCAGGGTGTTCGGAGC 501
QY 121 ACGGTCAAGCAAGTGACCTTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 180
DB 502 ACGGTCAAGCAAGTGACCTTTTCAGAGGTGGAGAGCCAGATTTCATCAATGACTGG 561
QY 181 GTGAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
DB 562 GTGAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 621
QY 241 CTGACACGGCTGTGCTGGTGAATGCTCTACTTCAACGGCCAGTGAAGACTCCCTTC 300
DB 622 CTGACACGGCTGTGCTGGTGAATGCTCTACTTCAACGGCCAGTGAAGACTCCCTTC 681
QY 301 CCGGACTCCAGCACCCACCGCGCCCTCTTCCAAATCAGACGGCAGCACTGTCTGTG 360
DB 682 CCGGACTCCAGCACCCACCGCGCCCTCTTCCAAATCAGACGGCAGCACTGTCTGTG 741
QY 361 CCCATGATGGCTCAGACCAACAGTTCAACTATCTAGTTTCCACCGCCGATGGCCAT 420
DB 742 CCCATGATGGCTCAGACCAACAGTTCAACTATCTAGTTTCCACCGCCGATGGCCAT 801
QY 421 TACTACGACATCTGGAACTGGCCCTACACGGGGACACCCCTCAGCATGTTCAATTGCTGC 480
DB 802 TACTACGACATCTGGAACTGGCCCTACACGGGGACACCCCTCAGCATGTTCAATTGCTGC 861
QY 481 CTTTATGAAAAAGAGTGCTCTCTGCTCCCTCACCAACATTCTGAGTGCCCGAGCTCATC 540
DB 862 CTTTATGAAAAAGAGTGCTCTCTGCTCCCTCACCAACATTCTGAGTGCCCGAGCTCATC 921
QY 541 AGCCACTGGAAGGCA 556
DB 922 AGCCACTGGAAGGCA 937

RESULT 12
US-10-197-258-1
; Sequence 1, Application US/10197258
; Publication No. US20040014190A1
; GENERAL INFORMATION:
; APPLICANT: LAWRENCE, DANIEL A.
; APPLICANT: GORLATOVA, NATALIA
; APPLICANT: CRANDALL, DAVID L.
; TITLE OF INVENTION: MUTANT PROTEINASE-INHIBITORS AND USES THEREOF
; FILE REFERENCE: 030523-0187
; CURRENT APPLICATION NUMBER: US/10/197,258
; CURRENT FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS


```
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1187:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2876 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g189541
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1187 :
US-10-641-643-1187

Query Match          100.0%; Score 556; DB 7; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCATGGAACAAAGGATGAGATCAGCACACAGACGCGATCTTCGTC 60
Db 382 AAGGAGCTCATGGGCGCATGGAACAAAGGATGAGATCAGCACACAGACGCGATCTTCGTC 441

QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120
Db 442 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 501

QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTTCATCATCAATCACTGG 180
Db 502 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTTCATCATCAATCACTGG 561

QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
Db 562 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 621

QY 241 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 622 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 681

QY 301 CCCGACTCCAGCACCCACCGCGCTCTTCCAAAATCAGACGGCAGCACTGTCTGTG 360
Db 682 CCCGACTCCAGCACCCACCGCGCTCTTCCAAAATCAGACGGCAGCACTGTCTGTG 741

QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGTTTCAACCGCCCGATGGCCAT 420
Db 742 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGTTTCAACCGCCCGATGGCCAT 801

QY 421 TACTACGACATCTTGGAACTGCCCTTACACGGGGACACCCCTCAGCATGTTCAATTGCTGC 480
Db 802 TACTACGACATCTTGGAACTGCCCTTACACGGGGACACCCCTCAGCATGTTCAATTGCTGC 861

QY 481 CCTTATGAAAAAGAGTGCTCTCTCTGCGCTCACCACAACTTCTGAGTCCCGAGCTCATC 540
Db 862 CCTTATGAAAAAGAGTGCTCTCTCTGCGCTCACCACAACTTCTGAGTCCCGAGCTCATC 921

QY 541 AGCCACTGGAAGGCA 556
Db 922 AGCCACTGGAAGGCA 937
```

```
RESULT 15
US-10-956-157-442
/ Sequence 442, Application US/10956157
/ Publication No. US20050118625A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
/ TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
/ FILE REFERENCE: 031896-043000 (AM 101081)
```

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/ CURRENT APPLICATION NUMBER: US/10/956,157
/ CURRENT FILING DATE: 2004-10-04
/ NUMBER OF SEQ ID NOS: 319805
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 442
/ LENGTH: 2876
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-956-157-442

Query Match          100.0%; Score 556; DB 9; Length 2876;
Best Local Similarity 100.0%; Pred. No. 4.7e-166;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCGCATGGAACAAAGGATGAGATCAGCACACAGACGCGATCTTCGTC 60
Db 382 AAGGAGCTCATGGGCGCATGGAACAAAGGATGAGATCAGCACACAGACGCGATCTTCGTC 441

QY 61 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120
Db 442 CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 501

QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTTCATCATCAATCACTGG 180
Db 502 ACGGTCAAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTTCATCATCAATCACTGG 561

QY 181 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 240
Db 562 GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGGACCA 621

QY 241 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 622 CTGACACGGCTGGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 681

QY 301 CCCGACTCCAGCACCCACCGCGCTCTTCCAAAATCAGACGGCAGCACTGTCTGTG 360
Db 682 CCCGACTCCAGCACCCACCGCGCTCTTCCAAAATCAGACGGCAGCACTGTCTGTG 741

QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGTTTCAACCGCCCGATGGCCAT 420
Db 742 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGTTTCAACCGCCCGATGGCCAT 801

QY 421 TACTACGACATCTTGGAACTGCCCTTACACGGGGACACCCCTCAGCATGTTCAATTGCTGC 480
Db 802 TACTACGACATCTTGGAACTGCCCTTACACGGGGACACCCCTCAGCATGTTCAATTGCTGC 861

QY 481 CCTTATGAAAAAGAGTGCTCTCTCTGCGCTCACCACAACTTCTGAGTCCCGAGCTCATC 540
Db 862 CCTTATGAAAAAGAGTGCTCTCTCTGCGCTCACCACAACTTCTGAGTCCCGAGCTCATC 921

QY 541 AGCCACTGGAAGGCA 556
Db 922 AGCCACTGGAAGGCA 937
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Search completed: March 10, 2006, 01:43:32
Job time : 675 secs

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 10, 2006, 01:21:06 ; Search time 322 Seconds
(without alignments)
3984.028 Million cell updates/sec

Title: US-10-686-428A-4_COPY_238_793

Perfect score: 556
Sequence: 1 aagagctcatggggccatg.....catcagccactggaaggca 556

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:

- 1: /cgn2_5/ptodata/1/pubpna/US08_NEW_PUB.seq:
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
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- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	1209	8	US-10-821-234-729
2	556	100.0	2522	12	US-11-094-519A-11
3	556	100.0	2876	12	US-11-091-883-114
4	556	100.0	2937	8	US-10-775-169-229
5	556	100.0	3273	12	US-11-091-883-113
6	479	86.2	2438	12	US-11-094-519A-10
7	421.6	75.8	3053	12	US-11-136-527-3753
8	166.8	30.0	1404	8	US-10-750-185-46781
9	166.8	30.0	1404	8	US-10-750-623-46781
10	165.6	29.8	14302	12	US-11-136-527-3649
11	114	20.5	1191	9	US-11-245-147-95
12	114	20.5	1197	8	US-10-821-234-636
13	114	20.5	2129	12	US-11-186-284-184
14	98.4	17.0	1212	9	US-11-245-147-20
15	94.6	17.0	1963	12	US-11-136-527-1947
16	71.8	12.9	1398	7	US-10-959-322-2
17	71.8	12.9	1736	8	US-10-995-561-409
18	71.8	12.9	1911	8	US-10-995-561-410
19	70.6	12.7	1400	12	US-11-136-527-6043
20	70.6	12.7	1900	8	US-10-775-169-49

21	70.6	12.7	1900	12	US-11-091-883-135	Sequence 135, App
22	69.8	12.6	2081	12	US-11-128-061-1036	Sequence 1036, App
23	69.8	12.6	2081	12	US-11-128-049-1036	Sequence 1036, App
24	69.2	12.4	1299	7	US-10-959-322-40	Sequence 40, Appl
25	69.2	12.4	1395	7	US-10-959-309-18	Sequence 18, Appl
26	69.2	12.4	1395	7	US-10-959-322-1	Sequence 1, Appl
27	69.2	12.4	1599	9	US-11-129-861-43	Sequence 43, Appl
28	69	12.4	1918	8	US-10-821-234-48	Sequence 48, Appl
29	67	12.1	257	12	US-11-128-061-404	Sequence 404, App
30	67	12.1	257	12	US-11-128-061-404	Sequence 404, App
31	67	12.1	257	12	US-11-128-049-404	Sequence 404, App
32	67	12.1	257	12	US-11-128-049-404	Sequence 404, App
33	65	11.7	1378	12	US-11-128-061-873	Sequence 873, App
34	65	11.7	1378	12	US-11-128-049-873	Sequence 873, App
35	64.8	11.7	1370	9	US-11-048-774-12	Sequence 12, App
36	64.8	11.7	1371	9	US-11-048-774-1	Sequence 1, Appl
37	64.4	11.6	1943	12	US-11-136-527-2587	Sequence 2587, App
38	60.2	10.8	201	8	US-10-995-561-10853	Sequence 10853, A
39	60.2	10.8	201	8	US-10-995-561-10866	Sequence 10866, A
40	59.4	10.7	1466	8	US-10-276-233A-14	Sequence 14, Appl
41	59.4	10.7	2480	9	US-11-072-512-1410	Sequence 1410, App
42	59	10.6	1606	8	US-10-995-561-278	Sequence 278, App
43	59	10.6	1655	8	US-10-995-561-277	Sequence 277, App
44	59	10.6	2480	8	US-10-995-561-276	Sequence 276, App
45	57.6	10.4	1690	12	US-11-136-527-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-10-821-234-729

; Sequence 729, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: pt_seq_genes Version 1.0

; SEQ ID NO 729

; LENGTH: 1209

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-821-234-729

Query Match	100.0%	Score 556;	DB 8;	Length 1209;
Best Local Similarity	100.0%;	Pred. No. 6.8e-150;		
Matches 556;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AAGGAGCTCATGGGCGCATGGAAACAGGATGAGATCAGCACACAGCGATCTTCGTC	60	
Db	307	AAGGAGCTCATGGGCGCATGGAAACAGGATGAGATCAGCACACAGCGATCTTCGTC	366	
QY	61	CAGCGGAGTCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCCTTCAGGGTGTTCGGGAGC	120	
Db	367	CAGCGGAGTCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCCTTCAGGGTGTTCGGGAGC	426	
QY	121	ACGGTCAAGCAAGTGAAGCTTTTCAGAGGTGGAGAGCCAGATTCATCAATCAATGCTGG	180	
Db	427	ACGGTCAAGCAAGTGAAGCTTTTCAGAGGTGGAGAGCCAGATTCATCAATCAATGCTGG	486	
QY	181	GTGAACACACACACAAAAGGTATGATCAGCACTTCTGGGAAGGAGCCGCTGGACACG	240	
Db	487	GTGAACACACACACAAAAGGTATGATCAGCACTTCTGGGAAGGAGCCGCTGGACACG	546	

241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
Db |||||
547 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 606
Qy |||||
301 CCGGACTCAGACACCGCCGCTCTTCCAAATCAGCGGAGGACTGTCTCTGTG 360
Db |||||
607 CCGGACTCAGACACCGCCGCTCTTCCAAATCAGCGGAGGACTGTCTCTGTG 666
Qy |||||
361 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACGCCCGATGGCCAT 420
Db |||||
667 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACGCCCGATGGCCAT 726
Qy |||||
421 TACTAGACATCCTGGAAGTCCCTACCAACGGGACACCCCTCAGCATGTTTCAATGCTGCC 480
Db |||||
727 TACTAGACATCCTGGAAGTCCCTACCAACGGGACACCCCTCAGCATGTTTCAATGCTGCC 786
Qy |||||
481 CTTTATGAAAAGAGTGGCTCTCTGCGCCTCACCAATCTCTAGTCCCGAGCTCATC 540
Db |||||
787 CTTTATGAAAAGAGTGGCTCTCTGCGCCTCACCAATCTCTAGTCCCGAGCTCATC 846
Qy |||||
541 AGCCACTGGAAGGCA 556
Db |||||
847 AGCCACTGGAAGGCA 862

RESULT 2

US-11-094-519A-11
; Sequence 11, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-094-519A-11

Query Match 100.0%; Score 556; DB 12; Length 2522;
Best Local Similarity 100.0%; Pred. No. 8.3e-150;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAGCTCATGGGCGCATGGAAACAAGGATGAGATCAGCACACAGACGCGATCTTGTGTC 60
Db 454 AAGGAGCTCATGGGCGCATGGAAACAAGGATGAGATCAGCACACAGACGCGATCTTGTGTC 513
Qy 61 CAGCGGATCTCAAGCTGGTCCAGGGCTTCATGCCCACTCTTCAGGCTGTTCGGAGC 120
Db 514 CAGCGGATCTCAAGCTGGTCCAGGGCTTCATGCCCACTCTTCAGGCTGTTCGGAGC 573
Qy 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGAGCCAGATTTCATCAATGACTGG 180
Db 574 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGAGCCAGATTTCATCAATGACTGG 633
Qy 181 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGGAAAGGAGCCGTGGACCAAG 240
Db 634 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGTGGAAAGGAGCCGTGGACCAAG 693
Qy 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
Db 694 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 753
Qy 301 CCCGACTCCAGCACCCACCGCGCCTCTTCCAAATCAGACGGGAGCAGTGTCTCTGTG 360

754 CCCGACTCCAGCACCCACCGCGCCTCTTCCAAATCAGACGGCAGCAGTGTCTCTGTG 813
Qy |||||
361 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACGCCCGATGGCCAT 420
Db |||||
814 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCAACACGCCCGATGGCCAT 873
Qy |||||
421 TACTAGACATCCTGGAAGTCCCTACCAACGGGACACCCCTCAGCATGTTTCAATGCTGCC 480
Db |||||
874 TACTAGACATCCTGGAAGTCCCTACCAACGGGACACCCCTCAGCATGTTTCAATGCTGCC 933
Qy |||||
481 CTTTATGAAAAGAGTGGCTCTCTGCGCCTCACCAATCTCTAGTCCCGAGCTCATC 540
Db |||||
934 CTTTATGAAAAGAGTGGCTCTCTGCGCCTCACCAATCTCTAGTCCCGAGCTCATC 993
Qy |||||
541 AGCCACTGGAAGGCA 556
Db |||||
994 AGCCACTGGAAGGCA 1009

RESULT 3

US-11-091-883-114
; Sequence 114, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: PERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN
; TITLE OF INVENTION: VIABILITY
; FILE REFERENCE: 539420S
; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-091-883-114

Query Match 100.0%; Score 556; DB 12; Length 2876;
Best Local Similarity 100.0%; Pred. No. 8.6e-150;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAGCTCATGGGCGCATGGAAACAAGGATGAGATCAGCACACAGACGCGATCTTGTGTC 60
Db 382 AAGGAGCTCATGGGCGCATGGAAACAAGGATGAGATCAGCACACAGACGCGATCTTGTGTC 441
Qy 61 CAGCGGATCTCAAGCTGGTCCAGGGCTTCATGCCCACTCTTCAGGCTGTTCGGAGC 120
Db 442 CAGCGGATCTCAAGCTGGTCCAGGGCTTCATGCCCACTCTTCAGGCTGTTCGGAGC 501
Qy 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGAGCCAGATTTCATCAATGACTGG 180
Db 502 ACGGTCAAGCAAGTGGACTTTTTCAGAGTGGAGAGAGCCAGATTTCATCAATGACTGG 561
Qy 181 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGGAAAGGAGCCGTGGACCAAG 240
Db 562 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGTGGAAAGGAGCCGTGGACCAAG 621
Qy 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 300
Db 622 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAGACTCCCTTC 681
Qy 301 CCCGACTCCAGCACCCACCGCGCCTCTTCCAAATCAGACGGGAGCAGTGTCTCTGTG 360
Db 682 CCCGACTCCAGCACCCACCGCGCCTCTTCCAAATCAGACGGGAGCAGTGTCTCTGTG 741

Qy	361	CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTAGTTCACCAAGCCCGATGGCCAT	420
Db	742	CCCATGATGGCTCAGACCAACAAGTTCAACTATATCTAGTTCACCAAGCCCGATGGCCAT	801
Qy	421	TACTACGACATCCTGGAACTGCCCTTACCACGGGGACACCCCTCAGCATGTTCATTGCTGCC	480
Db	802	TACTACGACATCCTGGAACTGCCCTTACCACGGGGACACCCCTCAGCATGTTCATTGCTGCC	861
Qy	481	CCTTATGAAAAAGAGGTGCTCTCTCTGCCCTCACCACAACTTCTAGTGCCCGAGCTCATC	540
Db	862	CCTTATGAAAAAGAGGTGCTCTCTCTGCCCTCACCACAACTTCTAGTGCCCGAGCTCATC	921
Qy	541	AGCCACTGGAAGGCA	556
Db	922	AGCCACTGGAAGGCA	937

RESULT 4

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US-10-775-169-229
; Sequence 229, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 229
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-229

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Query Match	100.0%	Score 556;	DB 8;	Length 2937;
Best Local Similarity	100.0%;	Pred. No. 8.7e-150;		
Matches 556;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AAGGAGCTCATGGGGCCATGGAA	CAGGATGAGATCAGCAC	CAGACGCGATCTTCGTC 60
DB	250	AAGGAGCTCATGGGGCCATGGAA	CAGGATGAGATCAGCAC	CAGACGCGATCTTCGTC 309
QY	61	CAGCGGATCTGAAGCTGGTCC	AGGGTTTCATGCCCATCTTCT	CAGGCTGTCGCGAGC 120
DB	310	CAGCGGATCTGAAGCTGGTCC	AGGGTTTCATGCCCATCTTCT	CAGGCTGTCGCGAGC 369
QY	121	ACGGTCAAGCAAGTGGACTTTT	CAGAGTGGAGAGCCAGATT	CATCATCAATGACTGG 180
DB	370	ACGGTCAAGCAAGTGGACTTTT	CAGAGTGGAGAGCCAGATT	CATCATCAATGACTGG 429
QY	181	GTGAAGACACACAAAGATGAT	CAGCAACTTGCTTGGGAAAG	AGCCCGTGGACCAAG 240
DB	430	GTGAAGACACACAAAGATGAT	CAGCAACTTGCTTGGGAAAG	AGCCCGTGGACCAAG 489
QY	241	CTGACACGGCTGGTGTGGTA	TGCCCTCTACTTCAACGGCC	AGTGGAGACTCCCTTC 300
DB	490	CTGACACGGCTGGTGTGGTA	TGCCCTCTACTTCAACGGCC	AGTGGAGACTCCCTTC 549
QY	301	CCGGAATCCAGCACCCACCG	CGCCCTTCCACAAATCAG	AGCGCAGCACTGTCTCTG 360
DB	550	CCGGAATCCAGCACCCACCG	CGCCCTTCCACAAATCAG	AGCGCAGCACTGTCTCTG 609
QY	361	CCCATATGGCTCAGACCCACA	AGTTCAACTATACTAGTTC	CACACGCCCGCATGGCCAT 420
DB	610	CCCATATGGCTCAGACCCACA	AGTTCAACTATACTAGTTC	CACACGCCCGCATGGCCAT 669
QY	421	TACTACGACATCTCGGAATG	CCCTACACGGGACACCCCT	CAGATGTTCAATGCTGCC 480

Db	670	TACTACGACATCTCTGGAACCTCCCTACCAAGGGGACACCTCAGCATGTTTCATTGCTGCC	720
Qy	481	CCATTATGAAAAAGAGGTGCCTCTCTCTGCGCCCTCACCAACATTTCTGAGTGCCCGAGCTCATC	540
Db	730	CCATTATGAAAAAGAGGTGCCTCTCTCTGCGCCCTCACCAACATTTCTGAGTGCCCGAGCTCATC	789
Qy	541	AGCCACTGGAAAGGCA 556	
Db	790	AGCCACTGGAAAGGCA 805	
RESULT 5			
US-11-091-883-113			
; Sequence 113, Application US/11091883			
; Publication No. US20060024693A1			
; GENERAL INFORMATION:			
; APPLICANT: CIBELLI, JOSE			
; APPLICANT: FERNANDEZ, EMILIO O.			
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME			
; APPLICANT: KOCABAS, ARIF			
; APPLICANT: CROSBY, JAVIER A.			
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION			
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL			
; TITLE OF INVENTION: VIABILITY			
; FILE REFERENCE: 5394205			
; CURRENT APPLICATION NUMBER: US/11/091.883			
; CURRENT FILING DATE: 2005-03-29			
; PRIOR APPLICATION NUMBER: 60/556,875			
; PRIOR FILING DATE: 2004-03-29			
; NUMBER OF SEQ ID NOS: 513			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 113			
; LENGTH: 3273			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: modified_base			
; LOCATION: (23)..(25)			
; OTHER INFORMATION: a, c, g, or t			
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; NAME/KEY: modified_base			
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OTHER INFORMATION: a, c, g, or t
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NAME/KEY: modified_base
LOCATION: (2300)..(2300)
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NAME/KEY: modified_base
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NAME/KEY: modified_base
LOCATION: (3179)..(3182)
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LOCATION: (3243)..(3243)
OTHER INFORMATION: a, c, g, or t
US-11-091-883-113

Query Match 100.0%; Score 556; DB 12; Length 3273;

Best Local Similarity 100.0%; Pred. No. 8.9e-150;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGCCCATGGAAACAAGGATGAGATCAGCACACAGACGCGATCTTCGTC 60
DB 454 AAGGAGCTCATGGGCCCATGGAAACAAGGATGAGATCAGCACACAGACGCGATCTTCGTC 513
QY 61 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
DB 514 CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 573
QY 121 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCAGAGTTCATCATCAATGACTGG 180
DB 574 ACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCAGAGTTCATCATCAATGACTGG 633
QY 181 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGACCCAG 240
DB 634 GTGAAGACACACAAAAAGGTATGATCAGCAACTTGTGGGAAAGGAGCCGTGACCCAG 693
QY 241 CTGACACGGCTGGTCTGGTGAATGCCCTCTACTTTCACGGCCAGTGGAGACTCCCTTC 300
DB 694 CTGACACGGCTGGTCTGGTGAATGCCCTCTACTTTCACGGCCAGTGGAGACTCCCTTC 753
QY 301 CCGGACTCCAGCACCCACCGCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 360
DB 754 CCGGACTCCAGCACCCACCGCGCGCTCTTCCAAATCAGACGGCAGCACTGTCTCTGTG 813
QY 361 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGATTCCACCGCCGATGGCCAT 420
DB 814 CCCATGATGGCTCAGACCAACAAGTTCAACTATCTAGATTCCACCGCCGATGGCCAT 873
QY 421 TACTACGACATCTCGAACTGCCCTTACCACGGGACACCTTCAGCATGTTCAATTCGTC 480
DB 874 TACTACGACATCTCGAACTGCCCTTACCACGGGACACCTTCAGCATGTTCAATTCGTC 933
QY 481 CCTTATGAAAAAGAGGTGCTCTCTCTGCCCTCACCACATTCAGTCCCGAGCTCATC 540
DB 934 CCTTATGAAAAAGAGGTGCTCTCTCTGCCCTCACCACATTCAGTCCCGAGCTCATC 993
QY 541 AGCCACTGGAAAGGCA 556
DB 994 AGCCACTGGAAAGGCA 1009

RESULT 6
US-11-094-519A-10
; Sequence 10, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52


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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2438
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-094-519A-10

Query Match
 86.2%; Score 479; DB 12; Length 2438;
Best Local Similarity 100.0%; Pred. No. 1.1e-127;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGAAACAAAGGATGAGATCAGACACACAGACGCGATCTTCGTC 60
DB 454 AAGGAGCTCATGGGGCCATGAAACAAAGGATGAGATCAGACACACAGACGCGATCTTCGTC 513
QY 61 CAGCGGAGCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTTCAGGGCTGTTCGGAGC 120;
DB 514 CAGCGGAGCTGAAGCTGTGTCAGGGCTTCATGCCCACTTCTTCAGGGCTGTTCGGAGC 573
QY 121 AGGTCACGCAAGTGCATCTTTCAGAGTGGAGAGCCAGATTCATCATCATGACTGG 180
DB 574 AGGTCACGCAAGTGCATCTTTCAGAGTGGAGAGCCAGATTCATCATCATGACTGG 633
QY 181 GTGAAGACACACAAAGATGATGATCAGCAACTTCTTGGGAAAGAGCCGTTGGACAC 240
DB 634 GTGAAGACACACAAAGATGATGATCAGCAACTTCTTGGGAAAGAGCCGTTGGACAC 693
QY 241 CTGACACGGCTGTGCTGGTGAATGCTCTTCAACGGCCAGTGGAGAGCTCCCTTC 300
DB 694 CTGACACGGCTGTGCTGGTGAATGCTCTTCAACGGCCAGTGGAGAGCTCCCTTC 753
QY 301 CCGGACTCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCTGTCTCTGTG 360
DB 754 CCGGACTCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCTGTCTCTGTG 813
QY 361 CCCATGATGGCTCAGACCAAGTTCACAAATCAGACGGCAGCTGTCTCTGTG 420
DB 814 CCCATGATGGCTCAGACCAAGTTCACAAATCAGACGGCAGCTGTCTCTGTG 873
QY 421 TACTACGATCCTGGAATCGCTTACCGGGGACACCTCAGCATGTTTCATTTGCTGC 479
DB 874 TACTACGATCCTGGAATCGCTTACCGGGGACACCTCAGCATGTTTCATTTGCTGC 932

RESULT 7
US-11-136-527-3753
; Sequence 3753, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3753
; LENGTH: 3053
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3753

Query Match
 75.8%; Score 421.6; DB 12; Length 3053;
Best Local Similarity 84.9%; Pred. No. 3.8e-111;
Matches 472; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGAAACAAAGGATGAGATCAGACACACAGACGCGATCTTCGTC 60
DB 425 AAGGAGCTCATGGGGCCATGAAACAAAGGATGAGATCAGACACACAGACGCGATCTTCGTC 484
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QY 61 CAGCGGATCTGAAGCTGTTCAGGGCTTCATGCCCCCACTCTTTCAGGCTGTTCGGAGC 120
DB 485 CAGCGGACCTAGAGCTGTTCAGGGCTTCATGCCCCCACTCTTTCAGGCTGTTCGGAGC 544
QY 121 ACGGTCACGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCATCAATGACTGG 180
DB 545 ACGGTCACGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTCATCATCAATGACTGG 604
QY 181 GTGAAGACACACAAAGATGATGATCAGCAACTTCTTGGGAAAGAGCCGTTGGACAC 240
DB 605 GTGAAGAGGACACACAAAGATGATGATCAGCAACTTCTTGGGAAAGAGCCGTTGGAC 664
QY 241 CTGACACGGCTGTGCTGTGATGCTCTTCAACGGCCAGTGGAGACTCCCTTC 300
DB 665 CTGACACGGCTGTGCTGTGATGCTCTTCAACGGCCAGTGGAGACTCCCTTC 724
QY 301 CCGGACTCAGCACCCACCGCGCTCTTCCACAAATCAGACGGCAGCTGTCTCTGTG 360
DB 725 TTAGAGGCGACAGCACCCACAGCGCTCTTCCAAAGTCTGATGTAGCACCATCTCCGTG 784
QY 361 CCCATGATGGCTCAGACCAAGTTCACAAATCAGACGGCAGCTGTCTCTGTG 420
DB 785 CCCATGATGGCTCAGACCAAGTTCACAAATCAGACGGCAGCTGTCTCTGTG 844
QY 421 TACTACGATCCTGGAATCGCTTACACGGGAGACCCCTCAGCATGTTTCATTTGCTGC 480
DB 845 GAGTACGATCCTGGAATCGCTTACACGGGAGACCCCTCAGCATGTTTCATTTGCTGC 904
QY 481 CCTTATGAAAGAGTGCCTCTCTGCGCTTCCACAAATCAGACGGCAGCTGTCTCTGTG 540
DB 905 CCTTATGAAAGAGTGCCTCTCTGCGCTTCCACAAATCAGACGGCAGCTGTCTCTGTG 964
QY 541 AGCCACTCGGAAAGGCA 556
DB 965 AGACAATGGAAGGCA 980

RESULT 8
US-10-750-185-46781
; Sequence 46781, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46781
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-46781

Query Match
 30.0%; Score 166.8; DB 8; Length 1404;
Best Local Similarity 85.3%; Pred. No. 5.5e-38;
Matches 186; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 194 CAAAGGATGATCAGCAACTTCTTGGGAAAGAGCCGTTGGACAGCTGTGACCGCTCG 253
DB 958 CCAATAGGATGATCAGCAACTTCTTGGGAAAGAGCCGTTGGACAGCTGTGACCGCTCG 1017
QY 254 TCGTGGTGAATGCTCTTCTTCAACGGCAGTGGAGACTCCCTTCCCGACTCCAGCA 313
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Db 1018 TCCTGGTAAATGCCCTCTACTTTCAACGGCCAGTGGAAAGATGCCCTTCCAGAGTCAAAACA 1077
QY 314 CCACCGCGCCTCTTCCAAATCAGACGGCAGCAGCTCTCTCTGTGCCCATGATGGCTC 373
Db 1078 CCACACCGCCTCTTCCAAATCGATCGATGGCAGCAGCTCTCTGTGCCCATGATGGCTC 1137
QY 374 AGACCAACAAGTTCAACTATCTACTAGTTCCACACGCC 411
Db 1138 AGACCAACAAGTTCAACTATCTACTAGTTCCACACGCC 411
RESULT 9
US-10-750-623-46781
; Sequence 46781, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46781
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Bovine 19866880662738
US-10-750-623-46781
Query Match 30.0%; Score 166.8; DB 8; Length 1404;
Best Local Similarity 85.3%; Pred. No. 5.5e-38;
Matches 186; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 194 CAAAGGTATGATCAGCAATCTGTTGGAAAGAGCGCTGACACGAGTGCACGCGTGG 253
Db 958 CCATAGGCATGATCAGCGCTTACTTGGTGAAGGGCTGTGACAGCTGACACGCTGG 1017
QY 254 TCCTGGTGAATGCCCTCTACTTTCAACGGCCAGTGGAAAGTCCCTTCCCGACTCCAGCA 313
Db 1018 TCCTGGTAAATGCCCTCTACTTTCAACGGCCAGTGGAAAGATGCCCTTCCAGAGTCAAAACA 1077
QY 314 CCACCGCGCCTCTTCCAAATCAGACGGCAGCAGCTCTCTGTGCCCATGATGGCTC 373
Db 1078 CCACACCGCCTCTTCCAAATCGATCGATGGCAGCAGCTCTCTGTGCCCATGATGGCTC 1137
QY 374 AGACCAACAAGTTCAACTATCTACTAGTTCCACACGCC 411
Db 1138 AGACCAACAAGTTCAACTATCTACTAGTTCCACACGCC 411
RESULT 10
US-11-136-527-3649
; Sequence 3649, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2003-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3649
; LENGTH: 14302
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3649
Query Match 29.8%; Score 165.6; DB 12; Length 14302;
Best Local Similarity 88.2%; Pred. No. 2.3e-37;
Matches 180; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 AAGGAGCTCATGGGGCCATGGAAAGATGAGATCAGACACAGACGCGATCTTCGTC 60
Db 5159 AAGGAGCTCATGGGGCTCATGGAACAAGAAATGAGATCAGTACTGCGGACGCCATCTTTGTC 5218
QY 61 CAGCGGGATCTGAAGCTGCTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCCGGAGC 120
Db 5219 CAGCGGGACCTAGAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTTCTCCGGACC 5278
QY 121 ACGGTCAAGCAAGTGGACTTTTTCAGAGGTGGAGAGCCAGATTTCATCATCAATGACTGG 180
Db 5279 ACGGTGAAGCAGGTGGACTTCTTCAGAGGTGGAAAGAGCCAGATTTCATCATCAAGCACTGG 5338
QY 181 GTGAAGACACACACAAAAGGTATG 204
Db 5339 GTGGAGAGGCACACCAAAAGGTAGG 5362
RESULT 11
US-11-245-147-95
; Sequence 95, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; CURRENT FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 95
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-245-147-95
Query Match 20.5%; Score 114; DB 9; Length 1191;
Best Local Similarity 54.9%; Pred. No. 7.9e-23;
Matches 247; Conservative 0; Mismatches 200; Indels 3; Gaps 1;
QY 110 TGTTCGGAGCAGCGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCAGATTCATCA 169
Db 398 TGTTCAGTGTGAGTCCGGATGTGAATTTGAGAGTCCAGCCTCTGCTGTGATTCGA 457
QY 170 TCAATGACTGGTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGGAAAGGAG 229
Db 458 TCAATGCTATGGTTAAAAACGAAACAGGGATATGATTGACAACTCTGCTGTCCAGATC 517
QY 230 CCGTGA---CCAGCTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGCCACT 286
Db 518 TTAATTGATGGTGTGCTCACCAGACTGGTCTCGTCAACGCACTGATTATTTCAAGGGTCTGT 577

QY	287	GGAA	GACTCCCTTCCCGGACTCAGCACCCACCGCGGCTCTTCCACAAATCAGACGGCA	346
Db	578	GGAAATCA	CGGTTTCAACCCGAGAACACAAAGAAACGCACTTTCTGTGGCAGCCGACGGGA	637
QY	347	GCACTGTCTCTGTGCCATGATGGGTTCAGACCAACAAAGTTCAACTATATCTGAGTTTCACCA	406	
Db	638	AATCCTATCAAGTGC	CAATGCTGGCCAGCTCTCCGTGTTCCGGTGGGTGCGACAAGTG	697
QY	407	CGCCGATGGCCATTTATACGACATCTCTGGAACTGCCCTTACACCGGGGACACCTTCAGCA	466	
Db	698	CCCCCAATGATTTATGGTACAACTTCATTGAACTGCCCTTACCACCGGGGAAAGCATCAGCA	757	
QY	467	TGTTCAATGTCTCCCTTATGAAAAAGGTGCGCTCTCTCTGCGCCTCACCACATCTTCTGA	526	
Db	758	TGCTGATTGCATCGCGATGAGAGCTCCACTCCGCTGTCTGCCATCTCCACACATCA	817	
QY	527	GTGCCAGCTCATCAGCCACTGGAAAGGCA	556	
Db	818	GCACCAAGACCATACAGACTTGGATGAGCA	847	

RESULT 12

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US-10-821-234-636
; Sequence 636, Application US/10821234
; Publication No. US2005025114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462, 047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pct_SEQ_genes Version 1.0
; SEQ ID NO 636
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-636

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Query Match	20.5%;	Score 114;	DB 8;	Length 1197;
Best Local Similarity	54.9%;	Pred. No. 7.9e-23;		
Matches	247;	Conservative 0;	Mismatches 200;	Indels 3; Gaps 1;
QY	110	TGTTCCGAGCACGGTCAAGCAAGTGACATTTTCAGAGGTGGAGAGAGCCAGATTCATCA	169	
DB	398	TGTTCCAGTGTGAGGTCCGGAATGTGAACATTTGAGGATCCAGCCTCTGCCTGTGATTCCA	457	
QY	170	TCANTGACTGGGTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTGGGAAAGAG	229	
DB	458	TCAATGCAATGGGTTAAAAATGAAACACAGGATATGATTGACAACTCTGTGTCCCCAGATC	517	
QY	230	CCGTGGA---CCAGCTGACACGGCTGGTGTGTAATGCGCCTCTACTTCAACGCCAGT	286	
DB	518	TTATTGATGGTGTCTCACCAGACTGGTCTCTGTCGTCACAGCAGTGTATTTCAAGGGTCTGT	577	
QY	287	GGAAGACTCCCTTCCCGACTCCAGCACCCACCGCGCCTCTTCCACAAATCAGACGGCA	346	
DB	578	GGAATCAGGGTTCCAAACCGGAGAACACAAAGAAACGCATTTCTGTGGCAGCCGCGGA	637	
QY	347	GCACTGTCTGTGCCCATGATGCTCAGACCAACAAAGTTCAACTATCTACTGATGTTCCAC	406	
DB	638	AATCCTATCAAGTCCAAATGCTGCCAGTCTCCGTGTTCGGGTGGGGTCGACAAGTG	697	
QY	407	CGCCGATGGCAATTACTAGACATCTCTGAACTGCGCTACCAACCGGGACACCCCTCAGCA	466	
DB	698	CCCCCAATGATTATGTGTACAACTTCATGAACTGCCCTTACCACGGGGAAGCATCAGCA	757	
QY	467	TGTTCAATGCTGCCCTTATGAAAAGAGGTGCCTCTCTCTGCGCCTCACCACAACTTCGA	526	

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Db      758  TGCTGATTGCACCTGCGGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATCA 817
QY      527  GTGCCCACTCATCAGCCACTGGAAAGGCA 556
Db      818  GCACCAAGACCATAGACAGCTGGATGAGCA 847

RESULT 13
US-11-186-284-184
; Sequence 184, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 2129
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (210)...(1406)
US-11-186-284-184

```

Query Match	20.5%;	Score 114;	DB 12;	Length 2129;
Best Local Similarity	54.9%;	Pred. No. 9.3e-23;		
Matches 247;	Conservative	0;	Mismatches 200;	Indels 3; Gaps 1
QY	110	TGTTCCGGACCGGTCAACGCAAGTGGACTTTTCAGAGGTGGAGAGCCAGCATTCATCA	169	
Db	607			
QY	170	TCAATGACTGGGTGAAGACACACACAAAAGGTATGATCAGCAACTTCTGTTGGGAAGAGG	229	
Db	667			
QY	230	CGGTGA---CAGCTGACACGGCTGGTGTGGTGAATGCCCCCTACTTCAAAGGCCAGT	286	
Db	727	TTATTGATGGTGTGCTCACCCAGACTGGTCTCGTCAACGCAGTGTATTTCAAAGGGTCTGT	786	
QY	287	GGAAGACTCCCTTCCCGACTCCAGCAGCACCAACCGCCGCCTCTTCCACAAATCAGACCGCA	346	
Db	787	GGAAATACCGTTTCCAAACCCGGAGAACAAAGAAACGCACTTTCTGTTGGCAGCCGACGGGA	846	
QY	347	GCACCTCTCTGTGCCCCATGATGGCTCAGACCAACAAAGTTTCAACTATCTAGTTTCCACCA	406	
Db	847	AATCCCTATCAAGTGGCAATGCTGGCCAGCTCTCCGTGTTCCGGTGTGGGTGCACAAGTG	906	
QY	407	CGGCCGATGCCATTACTAGGACATCTGGAACTGGCCCTTACCAACGGGGAACACCCCTCAGCA	466	
Db	907	CCCCCAATGATTTATGGTGAACCTTCATTTGAATGGCCCTTACCAACGGGGAAGCATCAGCA	966	

QY 467 TGTTCATTCCTGCCCTTATGAAAGAGGTGCTCTCTCTGCTCCCTCACCACATTTCTGA 526
Db 967 TGCTGATTGCTGCGGACTGAGAGCTCCACTCCGCTGTCTGCCATCATCCACACATCA 1026
QY 527 GTGCCAGCTCATCAGCCACTGGAAAGGCA 556
Db 1027 GCACCAAGACCATAGACAGCTGGATGAGCA 1056

RESULT 14
US-11-245-147-20
; Sequence 20, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; CURRENT FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-245-147-20

Query Match 17.7%; Score 98.4; DB 9; Length 1212;
Best Local Similarity 52.9%; Pred. No. 2.4e-18;
Matches 235; Conservative 0; Mismatches 206; Indels 3; Gaps 1;
QY 110 TGTTCGGAGCAGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGCAGATTTCATCA 169
Db 409 TGTTTCAGTGTGAAGTGCAGAAATGGAATTTCCAGGACCCAGCCTCTGCTCTGAGTCCA 468
QY 170 TCAATGACTGGGTGAAGACACACACAAAAAGGTATGATCAGCAACTTGTCTT---GGGAAAG 226
Db 469 TCAATTTTGGGTCAAAAATGAGACCAGGGGCATGATTGATAACCTGCTTTCCCCAAATC 528
QY 227 GAGCGGTGACAGCTGACACGCTGGTGTGTGTAATGCCCTCTACTTCAACGGCCAGT 286
Db 529 TGATCGATGGTGGCCCTTACCAAGCTGGTCTCTCTGTTAATGCAAGTGTATTTCAGGGGTTTGT 588
QY 287 GGAAGACTCCCTTCCCGACTCCAGACCCACCGCGCTCTTCCCAAAATCAGACGGCA 346
Db 589 GGAAGTCTCGGTTTCAACAGAGAGACAAAGAAACGGACATTCGTGGCAGGTGATGGGA 648
QY 347 GCACTGCTCTGTGCCCCATGATGGCTCAGACCAACAAAGTTTCAACTATATCTGAGTTTCACCA 406
Db 649 AATCCTTACCAAGTACCATTGTTGGCTCAGCTCTCTGTGTTCCGCTCAGGGTCTACCAAG 708
QY 407 CGCCGATGGCCATTACTAGGACATCCTGGAACTGCCCTACCAAGGGGACACCTTCAGCA 466
Db 709 CCCGGAATGGCTTATGGTACAACTTCAATTGAGTGGCCCTTACCATGTGTGAGCATCAGCA 768
QY 467 TGTTCATTCGCTCCCTTATGAAAAGAGGTGCTCTCTCTGCTCCCTCACCACATTTCTGA 526
Db 769 TGCTGATCGCCCTGGCAACAGAGAGTCCACCCCACTGTCTGCCATCATCCCTTCATCA 828
QY 527 GTGCCAGCTCATCAGCCACTGGA 550

Db 829 CTACCAAGACCATTCGATAGCTGGA 852
RESULT 15
US-11-136-527-1947
; Sequence 1947, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AWI01086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1947
; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1947
Query Match 17.0%; Score 94.6; DB 12; Length 1963;
Best Local Similarity 49.3%; Pred. No. 3.4e-17;
Matches 263; Conservative 4; Mismatches 263; Indels 3; Gaps 1;
QY 21 GAACAAGGATGATGATCAGACACACAGACGCGGATCTTCGTCCAGCGGATCTGAAGCTGT 80
Db 309 GAATAAAGACATWTGACCGTGGCCAATGCTGTGTTGTTCAGGAATGGCTTTAAAAGTGA 368
QY 81 CCAGGGCTTCATGCCCCCACTTCTTCAGGCTGTTCGGGAGACGGTCAAGAGTGGACTT 140
Db 369 AGTGCTTTTGACGAAGAACAAAGAGGTGTTTCAGTGTGAAGTACAGAGTGTGAATT 428
QY 141 TTCAGAGGTGGAGAGAGCCAGATTTCATCAATCACTGGGTGAAGACACACACAAAAG 200
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QY 201 TATGATCAGCAACTTGTCTT---GGGAAAGAGCGCGTGGACAGCTGACACGGCTGTGTCT 257
Db 489 CATGATTGACACACTTACTTCCCNMAAAMWRAAMRATAGTGTCTTTACCAAACTGTCTCT 548
QY 258 GGTGAATGCCCTTACTTCAACGGCCAGTGGAAAGACTCCCTTCCCGACTCCAGCACCCA 317
Db 549 CGTTAACCGAGTGTATTTCAAGGGTTTGTGGAATATCCCGTTTCAACCTGAGAACACGA 608
QY 318 CCGCGCCCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGAC 377
Db 609 GAAACGGACCTTCGTGGCAGGTGATGGAAATCTCTACCAAGTACCATGCTAGCCAGCT 668
QY 378 CAACAAGTTTCAATATATGAGTTTCAACACGGCCGATGSCCAATTAAGACATCTGGA 437
Db 669 CTCCGTGTTCCGCTCTGGGTCTACCAAAACCCCAATGGCTTATGGTACAACTTCAATCA 728
QY 438 ACTGCCCTTACCAAGGGGACACCTCAGCATGTTTCAATTCGTCGCCCTTATGAAAAGAGGT 497
Db 729 GTACTCCCTTACCATGTGTGAGCATCAGCATGTTGATCGCCCTTGGCCAAAGAGAGTCCAC 788
QY 498 GCTCTCTCTGCGCTCACCACATTTCTGAGTGGCCAGCTTCATCAGCCACTGGA 550
Db 789 CCCACTGTCCGCTCATCCCTCATCATCAGTACCAAGACCATCATATAGTCTGA 841

Search completed: March 10, 2006, 01:54:22
Job time : 322 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 23:11:05 ; Search time 5640 Seconds
(without alignments)
4612.344 Million cell updates/sec

Title: US-10-686-428A-4_COPY_238_793
Perfect score: 556
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:.*
2: gb_est2:.*
3: gb_est3:.*
4: gb_est4:.*
5: gb_est5:.*
6: gb_est6:.*
7: gb_est7:.*
8: gb_est8:.*
9: gb_gss1:.*
10: gb_gss2:.*
11: gb_gss3:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	659	CN309034	CN309034 170004247
2	556	100.0	813	2 BG829624	BG829624 602763976
3	556	100.0	932	2 BE905905	BE905905 601495570
4	556	100.0	1027	5 BX396693	BX396693 BX396693
5	556	100.0	1168	10 AY402982	AY402982 Pan trogl
6	556	100.0	1209	10 AY402981	AY402981 Homo sapi
7	556	100.0	1474	4 CR614829	CR614829 full-length
8	555.6	100.0	1019	5 BX379573	BX379573 BX379573
9	555.6	100.0	1085	5 BX335507	BX335507 BX335507
10	555.2	100.0	1028	5 BX425037	BX425037 BX425037
11	554.4	99.7	1116	5 BX446279	BX446279 BX446279
12	550.8	99.1	817	3 BI870529	BI870529 603394394
13	550.2	99.0	894	6 CA489543	CA489543 AGENCOURT
14	549.2	98.8	1029	5 BX382561	BX382561 BX382561
15	545	98.0	749	2 BI224436	BI224436 602940982
16	545	98.0	829	6 CD609138	CD609138 560817410
17	545	98.0	1124	5 BX378424	BX378424 BX378424
18	544.6	97.9	832	5 BX379609	BX379609 BX379609
19	544.4	97.9	996	5 BX377975	BX377975 BX377975
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21	543.6	97.8	1093	5 BX356157	BX356157 BX356157
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23	543.4	97.7	975	1	AL545394	AL545394
24	542	97.5	971	5	BX417006	BX417006
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26	541.8	97.4	1010	5	BX340248	BX340248
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28	540.6	97.2	853	5	BX344504	BX344504
29	539	96.9	581	3	BP237212	BP237212
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32	532.8	95.8	1019	1	AL550303	AL550303
33	532	95.7	968	5	BX355763	BX355763
34	531.6	95.6	1107	5	BX424917	BX424917
35	530	95.3	681	6	CF132569	CF132569 UI-HF-PQO
36	529	95.1	960	5	BX335314	BX335314
37	526.6	94.7	948	5	BX381412	BX381412
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41	517	93.0	869	3	BQ218607	BQ218607 AGENCOURT
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ALIGNMENTS

RESULT 1
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LOCUS CN309034 659 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000424711627 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN309034
VERSION CN309034.1 GI:47325448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 659)
AUTHORS Brandenberger R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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FEATURES

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ORIGIN

Query Match 100.0%; Score 556; DB 7; Length 659;
Best Local Similarity 100.0%; Pred. No. 4.7e-141;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 58 AAGGAGCTCATGGGGCCATGGAAACAAAGGATGAGATCAGCACACAGACCGCATCTTCGTC 117
QY 61 CAGCGGGATCTGAAGCTGTGCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 120
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Db 238 GTGAAGACACACACAAAGGATGATGATCAGCAACTTGTCTGGGAAAGGACCGTGGACCA 297
QY 241 CTGACACCGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
Db 298 CTGACACCGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 357
QY 301 CCGGACTCCAGCACCCACCGCGGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 360
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QY 361 CCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCCACACGCCGATGCCAT 420
Db 418 CCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCCACACGCCGATGCCAT 477
QY 421 TACTACGACATCCTGGAATGCCCTTACACGGGGACACCTCAGCATGTTCAATGCTGCC 480
Db 478 TACTACGACATCCTGGAATGCCCTTACACGGGGACACCTCAGCATGTTCAATGCTGCC 537
QY 481 CCTTATGAAAAGAGTGCTCTCTGCGCCCTCACAACATTCAGTGGCCAGCTCATC 540
Db 538 CCTTATGAAAAGAGTGCTCTCTGCGCCCTCACAACATTCAGTGGCCAGCTCATC 597
QY 541 AGCCACTGGAAAGGCA 556
Db 598 AGCCACTGGAAAGGCA 613

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RESULT 2
LOCUS BG829624
DEFINITION 602763976F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4899139 5',
mRNA sequence.
ACCESSION BG829624
VERSION BG829624.1 GI:14177211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Place: LNCM1790 row: h column: 20
High quality sequence stop: 810.
Location/Qualifiers
1..813
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Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match 100.0%; Score 556; DB 2; Length 813;
Best Local Similarity 100.0%; Pred. No. 5e-141;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 210 CAGCGGGATCTGAAGCTGTGCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGAGC 269
QY 121 ACGGTCACAGCAAGTGGACTTTTCAGAGTGGAGAGCCAGATTTCATCATCAATGACTGG 180
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QY 181 GTGAAGACACACACAAAGGATGATGATCAGCAACTTGTCTGGGAAAGGACCGTGGACCA 240
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QY 241 CTGACACCGGCTGGTGTGTAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
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QY 301 CCGGACTCCAGCACCCACCGCGGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 360
Db 450 CCGGACTCCAGCACCCACCGCGGCTCTTCCACAAATCAGACGGCAGCACTGTCTGTG 509
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCCACACGCCGATGCCAT 420
Db 510 CCCATGATGGCTCAGACCAACAAAGTTCAACTATCTAGTTTCCACACGCCGATGCCAT 569
QY 421 TACTACGACATCCTGGAATGCCCTTACACGGGGACACCTCAGCATGTTCAATGCTGCC 480
Db 570 TACTACGACATCCTGGAATGCCCTTACACGGGGACACCTCAGCATGTTCAATGCTGCC 629
QY 481 CCTTATGAAAAGAGTGCTCTCTGCGCCCTCACAACATTCAGTGGCCAGCTCATC 540
Db 630 CCTTATGAAAAGAGTGCTCTCTGCGCCCTCACAACATTCAGTGGCCAGCTCATC 689
QY 541 AGCCACTGGAAAGGCA 556
Db 690 AGCCACTGGAAAGGCA 705

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RESULT 3
LOCUS BE905905
DEFINITION 601495570F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897737 5',
mRNA sequence.
ACCESSION BE905905
VERSION BE905905.1 GI:10399246
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 932)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9692 row: k column: 18
High quality sequence stop: 672.
Location/Qualifiers
1. .932
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

FEATURES
source

[illegible]

Db		609 AGCCACTGGAAGCA 624
RESULT_4		
EX396693		
LOCUS		
DEFINITION		1027 bp mRNA linear EST 29-APR-2004 clone CSODI021YN07 5-PRIME, mRNA sequence.
ACCESSION		BX396693
VERSION		BX396693
KEYWORDS		EST.
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1027) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On May 13, 2003 this sequence version replaced gi:30617070. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4412.f
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
FEATURES		
source		
		For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI021CG04QP1kc=4412.f . Location/Qualifiers 1..1027 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODI021YN07" /tissue type="PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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QY	121	ACGGTCAAGCAAGTGACACTTTTTCAGAGGTGGAGAGCCAGAGTTTCATCATCAATCACTGG	180	
Db	554	ACGGTCAAGCAAGTGACACTTTTTCAGAGGTGGAGAGCCAGAGTTTCATCATCAATCACTGG	613	
QY	181	GTGAAGACACACACAAAAGGTATGATCAGCAACTTGTCTTGGGAAAGGACCGGTGGACCAAG	240	
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QY	241	CTGACACGGCTCGTGTGCTGAATGCCCTCTACTTTCACGGGCCAGTGGAGACTCCCTTC	300	
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QY	481	CCCTATGAAAAAGAGGTGCCTCTCTCGCCCTACCAACATTCCTGAGTGCCACGTCATC	540		
Db	914	CCCTATGAAAAAGAGGTGCCTCTCTCGCCCTACCAACATTCCTGAGTGCCACGTCATC	973		
QY	541	AGCCACTGGAAAGGCA	556		
Db	974	AGCCACTGGAAAGGCA	989		
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LOCUS	AY402982	Pan troglodytes SERPINE1 gene, VIRTUAL TRANSCRIPT, partial			
DEFINITION	AY402982	sequence, genomic survey sequence.			
ACCESSION	AY402982	GI:39758965			
VERSION	AY402982.1				
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE	1	(bases 1 to 1168)			
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cartgill,M.				
TITLE	Infering nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2	(bases 1 to 1168)			
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cartgill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
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	/locus_tag="HCM1405"				
ORIGIN					
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Best Local Similarity	100.0%;	Pred. No. 5.6e-141;			
Matches 556;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Db	307	AAGGAGCTCATGGGCCATGGAACAAGGATGAGATCAGCACCAAGCGCATCTTCGTC	366		
QY	61	CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCCTCAGCTGTTCCGGAGC	120		
Db	367	CAGCGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCCTCAGCTGTTCCGGAGC	426		

Qy	121	ACGGTCAAGCAAGTGGAAGCTTTTCAGAGGTGGAGAGCCAGGATTCATCATCAATGACTGG	180
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Qy	181	GTGAAGACACACAAAAGGTATGATCAGCACTTCTGGGAAAGGAGCGGTGGACCAG	240
Db	487	GTGAAGACACACAAAAGGTATGATCAGCACTTCTGGGAAAGGAGCGGTGGACCAG	546
Qy	241	CTGACACGGCTGCTGTGGTAATGCCCTCTACTTCAACGGCCAGTGGAGAAGCTCCCTTC	300
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Qy	301	CCGACTCCAGCACCCACCGCCGCTCTTCCCAAATCAGACGGCAGCACTGTCTCTGTG	360
Db	607	CCGACTCCAGCACCCACCGCCGCTCTTCCCAAATCAGACGGCAGCACTGTCTCTGTG	666
Qy	361	CCCATGATGCTCAGACCAACAAGTTTCAATATACTAGTTTACCAACGCCGCAGTGCCCAT	420
Db	667	CCCATGATGCTCAGACCAACAAGTTTCAATATACTAGTTTACCAACGCCGCAGTGCCCAT	726
Qy	421	TACTTAGCACATCTCGAAGTCCCTACCAACGGGACACCCCTCAGCATGTTTCATTGCTGCC	480
Db	727	TACTTAGCACATCTCGAAGTCCCTACCAACGGGACACCCCTCAGCATGTTTCATTGCTGCC	786
Qy	481	CCTTATGAAAAAGAGTGCTCTCTCTGCGCTCACCAACATTTCTAGTGCCCGCAGCTCATC	540
Db	787	CCTTATGAAAAAGAGTGCTCTCTCTGCGCTCACCAACATTTCTAGTGCCCGCAGCTCATC	846
Qy	541	AGCCACTGGAAGGCA	556
Db	847	AGCCACTGGAAGGCA	862

RESULT 6
AY402981
LOCUS
DEFINITION Homo sapiens SRPINE1 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION AY402981
VERSION
KEYWORDS GSS.
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous gene trics
Science 302 (5652), 1960-1963 (2003)

TITLE
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES
source Location/Qualifiers
1..1209
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1209
/gene="SRPINE1"

gene

/locus_tag="HCM1405"

ORIGIN

Query Match 100.0%; Score 556; DB 10; Length 1209;
Best Local Similarity 100.0%; Pred. No. 5.6e-141;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAACAAAGATGAGATCAGCACACAGCGGATCTTCGTC 60
DB 307 AAGGAGCTCATGGGGCCATGGAACAAAGATGAGATCAGCACACAGCGGATCTTCGTC 366

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTCATGCCCACTTCTTCAGGCTGTTCGCGAGC 120
DB 367 CAGCGGATCTGAAGCTGGTCCAGGGTTCATGCCCACTTCTTCAGGCTGTTCGCGAGC 426

QY 121 ACGGTCAAGCAAGTGGATTTTCAGAGGTGGAGAGCCAGATTCATCATATGACTGG 180
DB 427 ACGGTCAAGCAAGTGGATTTTCAGAGGTGGAGAGCCAGATTCATCATATGACTGG 486

QY 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGGTGGACCCAG 240
DB 487 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGGTGGACCCAG 546

QY 241 CTGACAGGCTGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
DB 547 CTGACAGGCTGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 606

QY 301 CCGGACTCCAGACCCACCGCGGCTTTCACAAATCAGACGGGAGCACTGTCTGTG 360
DB 607 CCGGACTCCAGACCCACCGCGGCTTTCACAAATCAGACGGGAGCACTGTCTGTG 666

QY 361 CCCATGATGCTCAGACCAACAGTCACTACTTCAAGTTCACCGCCGAGTGGCCAT 420
DB 667 CCCATGATGCTCAGACCAACAGTCACTACTTCAAGTTCACCGCCGAGTGGCCAT 726

QY 421 TACTAGACATCTGGAACTGCCCTCACCAGGGGACACCCCTCAGCATGTTCAATGTCGC 480
DB 727 TACTAGACATCTGGAACTGCCCTCACCAGGGGACACCCCTCAGCATGTTCAATGTCGC 786

QY 481 CTTATGAAAGAGGTGCTCTCTGCGCTCACCACAAATTCAGTGGCCAGCTCATC 540
DB 787 CTTATGAAAGAGGTGCTCTCTGCGCTCACCACAAATTCAGTGGCCAGCTCATC 846

QY 541 AGCCACTGGAAAGGCA 556
DB 847 AGCCACTGGAAAGGCA 862

RESULT 7

CR614829 1474 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0D1031YB21 of Placenta Cot 25-normalized

DEFINITION

CR614829

ACCESSION

CR614829, 1 GI:50495636

KEYWORDS

HTC; CDS; cDNA.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1474)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1474)
Genoscope.

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT

- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

source

1..1474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1031YB21"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 100.0%; Score 556; DB 4; Length 1474;
Best Local Similarity 100.0%; Pred. No. 6e-141;
Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAACAAAGATGAGATCAGCACACAGCGGATCTTCGTC 60
DB 434 AAGGAGCTCATGGGGCCATGGAACAAAGATGAGATCAGCACACAGCGGATCTTCGTC 493

QY 61 CAGCGGATCTGAAGCTGGTCCAGGGTTCATGCCCACTTCTTCAGGCTGTTCGCGAGC 120
DB 494 CAGCGGATCTGAAGCTGGTCCAGGGTTCATGCCCACTTCTTCAGGCTGTTCGCGAGC 553

QY 121 ACGGTCAAGCAAGTGGATTTTCAGAGGTGGAGAGCCAGATTCATCATATGACTGG 180
DB 554 ACGGTCAAGCAAGTGGATTTTCAGAGGTGGAGAGCCAGATTCATCATATGACTGG 613

QY 181 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGGTGGACCCAG 240
DB 614 GTGAAGACACACACAAAGGTATGATCAGCAACTTGTCTGGAAAGGAGCGGTGGACCCAG 673

QY 241 CTGACAGGCTGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 300
DB 674 CTGACAGGCTGTGTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAAGACTCCCTTC 733

QY 301 CCGGACTCCAGACCCACCGCGGCTTTCACAAATCAGACGGGAGCACTGTCTGTG 360
DB 734 CCGGACTCCAGACCCACCGCGGCTTTCACAAATCAGACGGGAGCACTGTCTGTG 793

QY 361 CCCATGATGCTCAGACCAACAGTTCATCTACTACTACTACTACTACTACTACTACT 420
DB 794 CCCATGATGCTCAGACCAACAGTTCATCTACTACTACTACTACTACTACTACTACT 853

QY 421 TACTAGACATCTGGAACTGCCCTCACCAGGGGACACCCCTCAGCATGTTCAATGTCGC 480
DB 854 TACTAGACATCTGGAACTGCCCTCACCAGGGGACACCCCTCAGCATGTTCAATGTCGC 913

QY 481 CTTATGAAAGAGGTGCTCTCTGCGCTCACCACAAATTCAGTGGCCAGCTCATC 540
DB 914 CTTATGAAAGAGGTGCTCTCTGCGCTCACCACAAATTCAGTGGCCAGCTCATC 973

QY 541 AGCCACTGGAAAGGCA 556
DB 974 AGCCACTGGAAAGGCA 989

RESULT 8

LOCUS

DEFINITION

BX379573

ACCESSION

BX379573

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

BX379573 1019 bp mRNA linear EST 28-APR-2004
BX379573 Homo sapiens PLACENTA Cot 25-NORMALIZED Homo sapiens cDNA
clone CS0D1031YB21 5-PRIME, mRNA sequence.

BX379573
BX379573.2 GI:46832548
EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1. (bases 1 to 1019)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30450782.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4412.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI035CF07QPI&c=4412.f.

FEATURES
source

1..1019
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI035YL13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 100.0%; Score 556; DB 5; Length 1019;
Best Local Similarity 99.8%; Pred. No. 6.9e-141;
Matches 555; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAGATGATGATCAGCACACAGAGCGGATCTTCGTC 60
DB 432 AAGGAGCTCATGGGGCCATGGAAACAGATGATGATCAGCACACAGAGCGGATCTTCGTC 491
QY 61 CAGCGGATCTGAAGCTGGTCCAGAGCTTCATGCCCTCTTCAGAGCTGTTCCGGAGC 120
DB 492 CAGCGGATCTGAAGCTGGTCCAGAGCTTCATGCCCTCTTCAGAGCTGTTCCGGAGC 551
QY 121 ACGGTCAAGCAAGTGGATCTTTTCAGAGGTGGAGAGCGAGATTCATCAATCAATGACTGG 180
DB 552 ACGGTCAAGCAAGTGGATCTTTTCAGAGGTGGAGAGCGAGATTCATCAATCAATGACTGG 611
QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGAAAGGAGCGGTGACACAG 240
DB 612 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGAAAGGAGCGGTGACACAG 671
QY 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGGACGTGGAGACTCCCTTC 300
DB 672 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGGACGTGGAGACTCCCTTC 731
QY 301 CCGGACTCCAGCACACCGCGCTCTTCCACAAATCAGAGCGAGCACTGTCTCTGTG 360
DB 732 CCGGACTCCAGCACACCGCGCTCTTCCACAAATCAGAGCGAGCACTGTCTCTGTG 791
QY 361 CCCATGATGGCTCAGACCAACAAAGTTCAACTATATGATGTTCAACCGCGGATGCCAT 420
DB 792 CCCATGATGGCTCAGACCAACAAAGTTCAACTATATGATGTTCAACCGCGGATGCCAT 851
QY 421 TACTACGATCCTGGATCGCTCCCTACACGGGGACACCTTCAGATGTTCAATTCCTGCC 480
DB 852 TACTACGATCCTGGATCGCTCCCTACACGGGGACACCTTCAGATGTTCAATTCCTGCC 911
QY 481 CCTTATGAAAAGAGGTGCTCTCTCTGCCCTCACCACATTTCTGAGTGGCCAGCTCATC 540
DB 912 CCTTATGAAAAGAGGTGCTCTCTCTGCCCTCACCACATTTCTGAGTGGCCAGCTCATC 971
QY 541 AGCCACTGGAAGGCA 556

Db 972 AGCCACTGGAAGGCA 987

|||||||:|||||

RESULT 9
BX335507

LOCUS
DEFINITION
BX335507 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI015YB08 5-PRIME, mRNA sequence.
BX335507
ACCESSION
VERSION
BX335507.2 GI:46266450
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1085)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 1, 2003 this sequence version replaced gi:30312419.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4412.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI015DA04QPI&c=4412.f.

FEATURES
source

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/mol_type="mRNA"
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/clone="CS0DI015YB08"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 100.0%; Score 556; DB 5; Length 1085;
Best Local Similarity 99.8%; Pred. No. 7e-141;
Matches 555; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGAAACAGATGATGATCAGCACACAGAGCGGATCTTCGTC 60
DB 421 AAGGAGCTCATGGGGCCATGGAAACAGATGATGATCAGCACACAGAGCGGATCTTCGTC 480
QY 61 CAGCGGATCTGAAGCTGGTCCAGAGCTTCATGCCCTCTTCAGAGCTGTTCCGGAGC 120
DB 481 CAGCGGATCTGAAGCTGGTCCAGAGCTTCATGCCCTCTTCAGAGCTGTTCCGGAGC 540
QY 121 ACGGTCAAGCAAGTGGATCTTTTCAGAGGTGGAGAGCGAGATTCATCAATCAATGACTGG 180
DB 541 ACGGTCAAGCAAGTGGATCTTTTCAGAGGTGGAGAGCGAGATTCATCAATCAATGACTGG 600
QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGAAAGGAGCGGTGACACAG 240
DB 601 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTGGAAAGGAGCGGTGACACAG 660
QY 241 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGGACGTGGAGACTCCCTTC 300
DB 661 CTGACACGGCTGGTGGTGAATGCCCTCTACTTCAACGGGACGTGGAGACTCCCTTC 720
QY 301 CCGGACTCCAGCACACCGCGCTCTTCCACAAATCAGAGCGGAGCACTGTCTCTGTG 360

61	QY	CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC	120
498	Db	CAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCACTTCTTCAGGCTGTTCGGGAGC	557
121	QY	ACGGTCAAGCAAGTGACATTTTCAGAGGTGGAGAGGCCAGATTTCATCATCAATGACTGG	180
558	Db	ACGGTCAAGCAAGTGACATTTTCAGAGGTGGAGAGGCCAGATTTCATCATCAATGACTGG	617
181	QY	GTGAAGACACACAAAAGGTATGATCAGCAACTTCGTTGGGAAAGAGGCGGTGGACAG	240
618	Db	GTGAAGACACACAAAAGGTATGATCAGCAACTTCGTTGGGAAAGAGGCGGTGGACAG	677
241	QY	CTGACACGGCTGGTGTGCTGAATGCGCCTCTACTCAAACGGCCAGTGGAAAGACTCCCTTC	300
678	Db	CTGACACGGCTGGTGTGCTGAATGCGCCTCTACTCAAACGGCCAGTGGAAAGACTCCCTTC	737
301	QY	CCGCACTCCAGCACACCGCGCCTTCCTCCAAATCAGCGGCAGCACTGCTCTGTGG	360

OY	361	CCCATGATGGCTCAGACCAACAAGTTCAACTATAC	TGAGTTTACCACGCCCGATGGCCAT	420
Ddb	798	CCCATGATGGCTCAGACCAACAAGTTCAACTATAC	TGAGTTTACCACGCCCGATGGCCAT	857
OY	421	TACTTCGCATCTGTGGAACTGACCCCTAACACCGG	CCTCACACCTGCTCTTCTCTCTCTCTCTCTCTCTCT	480

858	TACTACGACATCCTGGAACTGCCCTACACGGGGACACCCCTCAGCATGTTCAATTGCTGCC	917
481	CCTTATGAAAAGAGGTGCTCTCTCTGCCCTCACCACAATTCCTGAGTGCCCAAGCTCATC	540
918	CCTTATGAAAARAGGTGCTCTCTCTGCCCTCACCACAATTCCTGAGTGCCCAAGCTCATC	977
541	AGCCACTGGAAGGCA	556
978	AGCCACTGGAARGGCA	993

RESULT 11

[illegible]

REFERENCE	1 (bases 1 to 1116)
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On May 15, 2003 this sequence version replaced gi:30780405. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life technologies.

FEATURES source

1. .ll116
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

This sequence belongs to sequence cluster 4412.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?S=XCL0BAA01ZE03RPI&c=4412.f>.
Location/Qualifiers

division of Invitrogen.
divided into two parts was constructed by nine technologies,

AGENCY: 10810368 MAPcL Homo sapiens cDNA clone IMAGE:6722018 5', mRNA sequence.

CA489543
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 894)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14284 row: b column: 02
High quality sequence stop: 674.

FEATURES
Location/Qualifiers
1..894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6722018"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, HERT-HME1, LNCAP"
/lab_host="EMDH10B"
/clone_lib="MAPcL"
/notes="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

ORIGIN
Query Match 99.0%; Score 550.2; DB 6; Length 894;
Best Local Similarity 99.5%; Pred. No. 2e-139;
Matches 552; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGGAACAAAGGATGAGATCAGCACACAGACCGCATCTTCGTC 60
DB 298 AAGGAGCTCATGGGGCCATGGGAACAAAGGATGAGATCAGCACACAGACCGCATCTTCGTC 357

QY 61 CAGCGGGATCTGAAGCTGTCAGGGCTTCATGCCCATCTTTCAGGCTGTTCGGAGC 120
DB 358 CAGCGGGATCTGAAGCTGTCAGGGCTTCATGCCCATCTTTCAGGCTGTTCGGAGC 417

QY 121 ACGGTCAAGCAAGTGAATTTTCAGAGGTGGAGAGCCAGATTTCATCATCAATGACTGG 180
DB 418 ACGGTCAAGCAAGTGAATTTTCAGAGGTGGAGAGCCAGATTTCATCATCAATGACTGG 477

QY 181 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGTGGACACAG 240
DB 478 GTGAAGACACACAAAAGGTATGATCAGCAACTTGTCTGGAAAGAGCCGTGGACACAG 537

QY 241 CTGACAGGCTGGTGTGTGATGTCCTCTACTTCAACGGCCAGTGGAAAGCTCCCTTC 300
DB 538 CTGACAGGCTGGTGTGTGATGTCCTCTACTTCAACGGCCAGTGGAAAGCTCCCTTC 597

QY 301 CCGGACTCCAGACACCCAGCCGCTCTTCCAAATCAGAGCGGAGCTGCTCTGTG 360
DB 598 CCGGACTCCAGACACCCAGCCGCTCTTCCAAATCAGAGCGGAGCTGCTCTGTG 657

QY 361 CCATGATGCTCAGACCAACAGTTCAACTACTACTGAGTTACACACGCCGATGCCAT 420
DB 658 CCATGATGCTCAGACCAACAGTTCAACTACTACTGAGTTACACACGCCGATGCCAT 717

QY 421 TACTAGACATCTGGAACCTGCCCTACACGGGGACACCTCAGCATGTTTATTGCTGCC 480
DB 718 TACTAGACATCTGGAACCTGCCCTACACGGGGACACCTCAGCATGTTTATTGCTGCC 777

QY 481 CTTATGAAAAGAGGTGCTCTCTGCTGCCTCACAACTTGTAGTGCCTCAGCTCATC 540
DB 778 CTTATGAAAAGAGGTGCTCTCTGCTGCCTCACAACTTGTAGTGCCTCAGCTCATC 837

QY 541 AGCCCTGGAAGGC 555
DB 838 AGCCCTGGAAGGC 852

RESULT 14
BX382561
LOCUS
DEFINITION
1029 bp mRNA linear EST 28-APR-2004
clone CS0D1082YB17 5-PRIME, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 1029)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30459067.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segrefgenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4412.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1082CA09QP1&c=4412.f.

FEATURES
Location/Qualifiers
1..1029
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1082YB17"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 98.8%; Score 549.2; DB 5; Length 1029;
Best Local Similarity 98.6%; Pred. No. 3.9e-139;
Matches 548; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAGCTCATGGGGCCATGGGAACAAAGGATGAGATCAGCACACAGACCGCATCTTCGTC 60
DB 437 AAGGAGCTCATGGGGCCATGGGAACAAAGGATGAGATCAGCACACAGACCGCATCTTCGTC 496

QY 61 CAGCGGGATCTGAAGCTGTCAGGGCTTCATGCCCATCTTTCAGGCTGTTCGGAGC 120
DB 497 CAGCGGGATCTGAAGCTGTCAGGGCTTCATGCCCATCTTTCAGGCTGTTCGGAGC 556

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QY 121 ACGGTCAAGCAAGTGAAGCTTTTTCAGAGTGGAGAGAGCCAGATTCATCATCAATCACTGG 180
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LOCUS 602940982F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5104076 5',
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ACCESSION BI224426
VERSION BI224426.1 GI:14677870
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 749)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11251 row: c column: 21
High quality sequence stop: 744.
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/clone="IMAGE:5104076"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
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ORIGIN
Query Match 98.0%; Score 545; DB 2; Length 749;
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Technologies."
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Search completed: March 10, 2006, 02:39:59
Job time : 5641 secs